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US-10-984-960A-20
US-10-893-576-39
US-10-805-177-12
US-10-805-177-12
US-10-805-177-12
US-10-802-088-98
US-10-292-088-70
US-10-822-306A-14
US-10-822-306A-14
US-10-822-306A-11
US-10-822-306A-11
US-10-822-306A-11
US-10-822-306A-11
US-10-292-088-142
US-10-292-088-66
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; Sequence 85, Application US/10735916A
; Publication No. US20050084906A1
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CRGANISM: Homo sapiens
US-10-735-916A-83
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US-10-735-916A-79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: DUFLOS, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: PC7/FR 03/00 538
PRIOR PELING DATE: 2003-01-10
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2002-01-18
PRIOR PELING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTIN VUMBER: FR 02/05 753
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 85
LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 625; DB 5; Best Local Similarity 100.0%; Pred. No. 5.8e-48; Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-85
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LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-735-916A-79
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                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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APPLICANT: GOETSCH, Liliane
APPLICANT: GOETSCH, Liliane
APPLICANT: GOETSCH, Liliane
APPLICANT: DUFLOS, Alain
APPLICANT: BEEK, Alain
APPLICANT: WOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
ITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
ITLE OF INVENTION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
PRIOR PRILING DATE: 2003-01-20
PRIOR PRILING DATE: 2003-01-18
PRIOR PRILING DATE: 2002-01-18
PRIOR PRILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
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Sequence 75, Application US/10735916A
Sequence 75, Application US/10735916A
Publication No. US20050084906A1
GENERAL INFORMATION:
APPLICANT: CORVIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HECW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
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  Length 117;
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                                                        1; Indels
Score 615; DB 5;
Pred. No. 3.9e-47;
1; Mismatches 1;
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Pred. No. 4.5e-47;
1; Mismatches 1
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98.4%;
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98.3%;
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Best Local Similarity 98.34
Matches 115; Conservative
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SOFTWARE: PatentIn Ver. 2.1
                                                        Matches 115; Conservative
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TYPE: PRT
CRGANISM: Homo sapiens
US-10-735-916A-81
Query Match
Best Local Similarity
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Sequence 77, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:

APPLICANT: GOETSCH, Liliane

APPLICANT: GOETSCH, Liliane

APPLICANT: CORVALA, Nathalie

APPLICANT: UEGER, Olivier

APPLICANT: HAEUW, Jean-Francois

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 01753-183

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 01753-183

CURRENT APPLICATION NUMBER: V8/10/735, 916A

CURRENT APPLICATION NUMBER: PCT/FR 03/00 178

PRIOR APPLICATION NUMBER: PCZ/PR 03/00 178

PRIOR APPLICATION NUMBER: FR 02/00 653

PRIOR APPLICATION NUMBER: FR 02/00 654

PRIOR PRILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18
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Best Local Similarity 96.6
Matches 113; Conservative
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US-10-735-916A-77
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ORGANISM: Homo sapiens
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US-10-735-916A-77
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i Sequence 143, Application US/10309762

i Publication No. US20040018198A1

i GENERAL INFORMATION:

APPLICANT: Galds, Jean

APPLICANT: Handa, Masahisa

APPLICANT: Gallo, Michael

ITLE OF INVENTION: (A.IX) TUMOR ANTIGEN

FILE REFERENCE: ABGENT: 0.27A

CURRENT APPLICATION NUMBER: US/10/309,762

CURRENT FILING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: 60/337275

PRIOR APPLICATION NUMBER: 60/337275

RIOR RILING DATE: 2001-12-03

NUMBER OF SEQ ID NOS: 246

SEQ ID NO 143

LENGTH: 119
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                                                                                                                                                                                                                                                                                                    Length 127;
                                                                                                                                                                                                                                                                                                                                               9; Indels
                                                                                                                                                                                                                                                                                                  Query Match

84.6%; Score 529; DB 5;
Best Local Similarity 82.8%; Pred. No. 1.9e-39;
Matches 96; Conservative 11; Mismatches 9.
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-05-07
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 52
                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-52
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ORGANISM: Homo sapiens
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US-10-292-088-109
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US-10-383-447-26

i Sequence 26, Application US/10383447

i Publication No. US20040096392A1

i GENERAL INFORMATION:

APPLICANT: Bhaskar, Vinay

APPLICANT: de la Calle, Agustin

APPLICANT: Caras, Ingrid

APPLICANT: Caras, Ingrid

APPLICANT: Amarkishnan, Vanitha

APPLICANT: Amarkishnan, Vanitha

APPLICANT: Afar, Daniel

APPLICANT: Afar, Daniel

APPLICANT: Afar, Daniel

APPLICANT: Afar, Daniel

APPLICANT: Murray, Richard

BRIOR FILING DATE: 2002-13-07

FRIOR FILING DATE: 2002-12-27

NUMBER OF SEQ ID NOS: 34

SOFTHWARE: PatentIn Version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCA---RYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDYGGNSYFDYWGQGTLVTVSS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIXYSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 514.5; DB 4; Length 118;
Pred. No. 3.5e-38;
3; Mismatches 11; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 82.3%; Score 514.5; DB 4; Length 120; I Similarity 82.4%; Pred. No. 3.5e-38; 98; Conservative 7; Mismatches 11; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Variable heavy chain region 3.0
                       FILE REFERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/10/292,088
CURRENT FILING DATE: 2003-03-14
FRIOR APPLICATION NUMBER: 60/348,980
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 109
LENGTH: 118
TITLE OF INVENTION: ANTIBODIES TO CD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.7<sup>3</sup>
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-109
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LENGTH: 120
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US-10-805-177-56

RESULT 12

Sequence 109, Application US/10292088
Publication No. US20030211100A1
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: CONVALAN, JOSE
APPLICANT: FENG, XIAO-CHI
APPLICANT: FENG, XIAO-CHI

; ;

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60 NPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARRGYDFLTGYDYFDYWGQGTLVT 119
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Sequence 128, Application US/10309762

Publication No. US20040018198A1

GENERAL INFORMATION:

APPLICANT: Gudas, Jean

APPLICANT: Handa, Masahisa

APPLICANT: Gallo, Michael

TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

TITLE OF INVENTION: ANTIBODIES

FILE REFERENCE: ABGENIX.027A

CURRENT FILING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: 60/337275

PRIOR APPLICATION NUMBER: 60/337275

PRIOR PELING DATE: 2001-12-03

NUMBER OF SEQ ID NOS: 246

SOFTWARE: FRALSE for Windows Version 4.0

SEQ ID NO 128
                                                                                                                                                                                                                                                                                                                                                                                                   US-10-309-762-29

US-10-309-762-29

Sequence 29, Application US/10309762

Publication No. US20040018198A1

GENERAL INPORMATION:

APPLICANT: Gudas, Jean

APPLICANT: Handa, Masahisa

APPLICANT: Handa, Masahisa

APPLICANT: Handa, Masahisa

APPLICANT: Handa, Masahisa

APPLICANT: APPLICANT: CAIX)

TITLE OF INVENTION: (CAIX) TUMOR ANTIGEN

TITLE OF INVENTION T
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61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVF
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; ORGANISM: Homo sapiens
US-10-309-762-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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US-10-309-762-128
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                                 Publication No. US20050084449A1

GENERAL INFORMATION:
APPLICANT: Chen, Francine
APPLICANT: Gazobeh, Binyam
APPLICANT: Gazobeh, Binyam
APPLICANT: Tee, Kam Fai
APPLICANT: Tee, Kam Fai
APPLICANT: Garzing, Medi
APPLICANT: Graning, Gary
APPLICANT: Graning, Gary
APPLICANT: Meses, Peter
APPLICANT: Meses, Peter
APPLICANT: Meses, Peter
APPLICANT: Meses, Peter
APPLICANT: Mramtsov, Nikolia
APPLICANT: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 YKPSLKDRVTISVDTSKNOPSLKLSSVTAADTAVYYCARYG--RVFFDYWGQGTLVTVSS 117
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Publication No. US20040018198A1
FRERRAL INFORMATION:
APPLICANT: Galds, Jean
APPLICANT: Foltz, Ian
APPLICANT: Holds, Jean
APPLICANT: Holds, Jean
APPLICANT: Holds, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT PILING DATE: 2002-12-02
FRIOR APPLICATION NUMBER: 60/337275
FRIOR APPLICATION NUMBER: 60/337275
FRIOR APPLICATION NUMBER: 60/337275
FRIOR APPLICATION NUMBER: 60/337275
FRIOR APPLICATION NUMBER: 246
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 122
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Sequence 56, Application US/10805177
Publication No. US20050084449A1
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Matches 103; Conservative
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; ORGANISM: Homo sapiens
US-10-309-762-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo Sapiens
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US-10-309-762-25
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LENGTH: 121
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        Query Match
        82.0%; Score 512.5; DB 4; Length 120;

        Best Local Similarity 85.0%; Pred: No. 5.3e-38;

        Matches 102; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

        Qy
        1 QVOLQESGPGLVKPSETLSLTCTVSGYS-ISGGYLWNWIRQPPGKGLEWIGYISYDGTNN 59

        Db
        1 QVOLGESGPGLVKPSETLSLTCTVSGSSVISGGYYWSWIRQPPGKGLEWIGYISYDGSSN 60

        QY
        60 YKPSIKDRVTISVDTSKNQPSLKLSSVTAADTAVYYCAR--YGRVPFDYWQGTLVTVSS 117

        Db
        61 YNPSIKSRVTISVDASKNQPSLKLSSVTAADTAVYYCARSWVRGVSFDYWQGTLVTVSS 120
```

Search completed: January 10, 2006, 21:35:33 Job time: 64.1754 secs

Sequence 1361, Ap Sequence 43, Appl Sequence 74, Appl Sequence 1510, Ap

1597, Appl 20, Appl 20, Appl 1981, Ap 1321, Appl 1221, Appl 1221, Appl 12, Appl 12, Appl 20, Appl 20,

Sequence Sequence Sequence Sequence Sequence

Sequence 1321, Sequence 1321,

1659, Ap 841, App 21, App 1607, Ap 1745, Ap 844, App 34, App 71, App 71, App

Sequence Seq

Sequence Sequence Sequence Sequence Sequence 2

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GENERAL INVORMATION:

APPLICANT: GOEYGCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HASUW, JEAN-FRANCOIS
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPPORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT PLILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-01-16
PRIOR PELICATION NUMBER: FR 020553
PRIOR APPLICATION NUMBER: FR 020553
PRIOR APPLICATION NUMBER: FR 0200553
PRIOR APPLICATION NUMBER: FR 0200554
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-01-18
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100.0%; Pred. No. 2.2e-48;
tive 0; Mismatches 0;
US-11-054-515-1659
US-11-054-515-841
US-11-054-515-1607
US-11-054-515-1607
US-11-054-515-1607
US-11-054-515-1745
US-10-054-515-184-34
US-10-512-184-71
US-10-512-184-71
US-11-054-515-1597
US-11-054-515-1981
US-11-054-515-1981
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US-11-054-515-1361
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                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 83, Application US/11012353; Publication No. US20050249730A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.4
Matches 117; Conservative
   ORGANISM: Homo sapiens
US-11-012-353-83
   US-11-012-353-83
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69, Appl
52, Appl
73, Appl
1651, Ap
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17, Appl
1994, Ap
1329, Ap
112, App
110, Appl
70, Appl
990, Appl
1339, Appl
                                                                                                            January 10, 2006, 20:55:23; Search time 5.96642 Seconds (without alignments) 166.558 Million cell updates/sec
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                                                                                                                                                                            US-10-735-916A-83
625
1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117
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1: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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US-11.012-353-75

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US-11.012-353-162

US-11.012-353-162

US-11.012-353-52

US-11.012-353-52

US-11.012-353-73

US-11.012-353-73

US-11.012-353-73

US-11.012-353-72

US-11.012-353-72

US-11.012-353-72

US-11.012-353-72

US-11.012-353-72

US-11.012-353-70

US-11.012-353-70
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                                                                                                                                                                                                                                                                                            61141 seqs, 8493638 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:

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NUMBER OF SEQ ID NOS: 162
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US-11-012-353-81
                                                                                                                              ; ORGANISM: Homo sapiens
US-11-012-353-79
                                                                                              LENGTH: 117
                                                                                                                 TYPE: PRT
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Sequence 79, Application US/11012353
Fublication No. US2005024973041
GENERAL INFORMATION:
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: BECK, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
FILE REFERENCE: 017753-196
FRIOR APPLICATION NUMBER: 10/735,916
FRIOR PELING DATE: 2003-07-11
FRIOR PELING DATE: 2003-07-11
FRIOR PELING DATE: 2003-01-20
FRIOR APPLICATION NUMBER: FR 0205753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLMNWIRQPPGKGLEWIGYISYDGTNNY 78
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ORGANISM: Homo sapiens
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US-11-02AVT: GORDERCH, NATHALIE
US-11-03AVT: LILIANE
US-11-03AVT: LIGER, OLIVIER
US-11-04-11-11-05 US-11-05
USEN-11-05 USEN-11-05-11-05
USEN-11-05-11-05-11-05-11-05
USEN-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11
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PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTIN Ver. 3.3
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SEQ ID NO 81
LENGTH: 135
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Gaps

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APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 01753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT PILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR PLICATION NUMBER: FR 020553
PRIOR FILING DATE: 2002-01-20
PRIOR PLICATION NUMBER: FR 0205653
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARR: PATCH FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
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Pred. No. 1.7e-41;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                       Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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97.8%; Score 611; DB 7;
Best Local Similarity 96.6%; Pred. No. 4.2e-47;
Matches 113; Conservative 3; Mismatches 1;
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR PELING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARR: PatentIn Ver. 3.3
SEQ ID NO 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 162, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HARUW, JEAN-FRANCOIS
APPLICANT: HARUW, JEAN-FRANCOIS
APPLICANT: HARUW, ABAN-FRANCOIS
APPLICANT: BECEK, ALAIN
APPLICANT: BECK, ALAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.4%;
88.0%;
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Best Local Similarity 88.04
Matches 103; Conservative
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US-11-012-353-162
                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-11-012-353-77
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                                                                                                                                                                                                                                              LENGTH: 135
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                                                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                     Sequence 75, Application Us/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DUFLOS, ALAIN

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILER REFERENCE: 011773-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT PILING DATE: 2004-12-16

PRIOR APPLICATION NUMBER: FR 0205753

PRIOR FILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 162

SSOFTWARE: PATENTIN VEV. 3.3
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APPLICANT: CORVAICH, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: BURLOS, ALAIN
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2003-12-16
PRIOR PILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
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Pred. No. 3.7e-47;
3; Mismatches 1;
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96.6%;
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; ORGANISM: Homo sapiens
US-11-012-353-75
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Best Local Similarity
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Best Local Similarity
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Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTCH, LILTANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LIGHT ANTI-IGF-IR AND JOSES THEREOF
FILER REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-12-16
PRIOR PELING DATE: 2003-07-11
PRIOR PELING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
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ARIOR FILING DATE: 2002-01-18
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Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GOETSCH, LILIANE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DUFLOS, ALAIN

APPLICANT: BECK, ALAIN

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REPERENCE: 017753-198

CURRENT APPLICATION NUMBER: 10/735,916

PRIOR APPLICATION NUMBER: 10/735,916

PRIOR APPLICATION NUMBER: 10/735,916

PRIOR APPLICATION NUMBER: PRO30538

PRIOR FILING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: PCT/FR03/00178
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61 NPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGOGTTLTVSS 117
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Best Local Similarity 82.8
Matches 96; Conservative
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; ORGANISM: Mus musculus
US-11-012-353-69
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APPLICANT: CORVAIA, NATHALIB
APPLICANT: CORVAIA, NATHALIB
APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
APPLICANT: BURLOS, ALAIN
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT PAPLICATION NUMBER: 10/735,916
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-01-20
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARR: PARCHIN VET. 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                  84.6%; Score 529; DB 7; Length 127; 82.8%; Pred. No. 5.4e-40;
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PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
NUMBER OF EQ ID NOS: 162
SOFTWARE: PAEGNIIN VET. 3.3
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Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96; Conservative
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ORGANISM: Homo sapiens
US-11-012-353-73
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US-11-012-353-52
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Sequence 72, Application US/11012353 Publication No. US20050249730A1 GENERAL INFORMATION:
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APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALIN
APPLICANT: HAEUW, JEAN FRANCOIS
APPLICANT: LEGER, OLIVIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 79.0%;
Matches 98; Conservative
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US-11-054-515-1548
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APPLICANT:
APPLICANT:
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61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARY-----GRVF-FDYWGQGTLV 113
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Fublication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
FRIOR PILING DATE: 2004-02-11
FRIOR APPLICATION NUMBER: 60/580,347
FRIOR FILING DATE: 2004-06-18
FRIOR FILING DATE: 2004-06-18
FRIOR FILING DATE: 2004-11-14
FRIOR FILING DATE: 2001-11-14
FRIOR FILING DATE: 2001-11-14
FRIOR FILING DATE: 2001-11-15
FRIOR FILING DATE: 2001-11-16
FRIOR FILING DATE: 2001-11-16
FRIOR FILING DATE: 2001-01-25
FRIOR FILING DATE: 2001-05-25
FRIOR FILING DATE: 2001-06-15
FRIOR FILING DATE: 2001-06-15
FRIOR FILING DATE: 2001-06-15
FRIOR FILING DATE: 2001-06-15
FRIOR FILING DATE: 2001-03-21
FRIOR FILING DATE: 2001-03-21
FRIOR FILING DATE: 2001-03-31
FRIOR FILING DATE: 2001-03-31
FRIOR FILING DATE: 2001-03-31
FRIOR FILING DATE: 2001-03-31
FRIOR FILING DATE: 2001-03-16
FRIOR FILING DATE: 2001-01-31-6
FRIOR FILING DATE: 2001-03-16
FRIOR FILING DATE: 2001-03-16
FRIOR FILING DATE: 2001-01-31-6
FRIOR FILING DATE: 2001-03-16
FRIOR FILING DATE: 2001-03-16
FRIOR FILING DATE: 2001-03-16
FRIOR FILING DATE: 2001-01-31-6
FRIOR FILING DATE: 2001-01-31-7
FRIOR FILING DATE: 2001-01-31-7
FRIOR FILING DATE: 2001-01-31-7
FRIOR FILING DATE: 2001-01-31-31-7
FRIOR FILING DATE: 2001-01-31-31-7
FRIOR FILING DATE: 2001-01-
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NUMBER OF SEQ ID NOS: 3247
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Sequence 1548, Application US/11054515

Publication No. US2005025533A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.6%; Score 491.5; DB 7; Length 247; 79.0%; Pred. No. 1.8e-36; Live 4; Mismatches 15; Indels 7
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Best Local Similarity 79.0°
Matches 98; Conservative
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; ORGANISM: Homo sapiens
US-11-054-515-1651
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61 NPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARVHYDILTGYLWAFDIWGQGTMV 120
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TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT PILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-10
PRIOR PILING DATE: 2003-01-10
PRIOR PILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
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PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR PLICATION NUMBER: 60/580,347
PRIOR PLICATION NUMBER: 10/293,418
PRIOR PLING DATE: 2004-06-18
PRIOR PLING DATE: 2001-11-14
PRIOR PLING DATE: 2001-11-16
PRIOR PLING DATE: 2001-11-16
PRIOR PLING DATE: 2001-12-19
PRIOR PLING DATE: 2001-12-19
PRIOR PLING DATE: 2001-12-19
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PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-0
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Pred. No. 1.9e-36;
5; Mismatches 14; Indels 7
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61 YNPSLKSRVTISIDTSKNQFSLKLSSVTAADTAVYYCVRSYYDILTGRPYTDAFDIWGKG 120
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Pred. No. 1.3e-35;
6; Mismatches 13; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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JOHNEAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523F3
CURRENT PAPPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR PILING DATE: 2004-02-11
PRIOR PILING DATE: 2004-02-11
PRIOR PILING DATE: 2004-02-11
PRIOR FILING DATE: 2004-02-13
PRIOR FILING DATE: 2004-06-18
PRIOR FILING DATE: 2004-06-18
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-01-15
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-16
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-16
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NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1619
                                                                                                                                                                                                                                                                                                                                                    DB 7; Length 117;
                                                                                                                                                                                                                                                                                                                                                    Score 483; DB 7; Length 11
Pred. No. 5e-36;
5; Mismatches 17; Indels
                                                                                                                                                                           FEATURE:

NAME/KEY: MOD RES

LOCATION: (59)

OTHER INFORMATION: Variable amino acid
US-11-012-353-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1619, Application US/11054515
Publication No. US20050255312A1
GENERAL INFORMATION:
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Best Local Similarity 81.2%;
Matches 95; Conservative !
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Best Local Similarity 77.2%;
Matches 98; Conservative
   NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 72
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US-11-054-515-1619
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US-11-054-515-1619
                                                                                                                        TYPE: PRT
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60 YKPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-----YGRVF---FDYMGQG 110

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1 QVQLQESGPGLVKPSETLSLTCTVSGYS-ISGGYLWNWIRQPPGKGLEWIGYISYDGTNN 59
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Pred. No. 1.2e-35;
2; Mismatches 18;
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
FILE REPERENCE: PH-1573-PCT
CURRENT APPLICATION NUMBER: US/10/721,763
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US/2001-150213
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-06-09
PRIOR FILING DATE: 2001-08-09
SRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-11
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PACENTIN VET: 2.1
SEQ ID NO 17
LENGTH: 146
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                                                                                                                                                                                                   ; Sequence 17, Application US/10721763; Publication No. US20050249729A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 82.2%;
Matches 97; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-721-763-17
111 TLVTVSS 117
                                                 121 TLVTVSS
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Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 11, Appl Sequence 64, Appl

OM protein

Run on:

Sequence:

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81.6%; Score 510; DB 2; Length 119;
85.0%; Pred. No. 2.8e-43;
iive 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New YORK

ZIP: 10021

ZIP: 10021

COUNTEX: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

PILING DATE: 18-FEB-1998

PRIOR APPLICATION NUMBER: EP 95 11 3021.0

PILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Halley, Jr., ESQ.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: Amino acids

TYPE: Amino acids
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STREET: 1251 Avenue of the Americas
CITY: New York
COUNTRY: New York
COUNTRY: New York
COUNTRY: New York
COUNTRY: New York
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Knappik, Achim
APPLICANT: Rappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
     US-08-480-774A-2

US-08-360-125-5

US-08-360-125-5

US-09-017-628-5

US-09-017-628-5

US-09-017-628-5

US-08-467-903-5

US-08-467-903-5

US-08-467-903-5

US-08-467-903-11

US-09-017-628-11

US-09-017-628-11

US-09-017-628-11

US-09-017-628-11

US-08-450-363-11

US-08-450-363-11

US-08-450-903-11

US-08-4137-117D-64

US-08-137-117D-64

US-08-137-117D-64

US-08-137-117D-64
                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                          US-09-025-769B-39; Sequence 39, Application US/09025769B; Sequence 39, Application US/09025769B; Patent No. 6300064; GENERAL INFORMATION:
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Best Local Similarity 85.0
Matches 102; Conservative
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MOLECULE TYPE: protein
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                          79, Appl
77, Appl
4, Appli
1, Appli
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Appl
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                                                                                             January 10, 2006, 20:34:27; Search time 22.847 Seconds (without alignments) 423.384 Million cell updates/sec
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65,
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/cgn2_6/ptodata/1/jaa/6_COMB.pep:*
/cgn2_6/ptodata/1/jaa/H_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/jaa/RB_COMB.pep:*
/cgn2_6/ptodata/1/jaa/RB_COMB.pep:*
              GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-025-769B-65
US-09-490-070A-39
US-09-490-153-65
US-09-490-153-65
US-09-490-153-65
US-09-490-153-65
US-09-090-324-65
US-09-025-769B-2
US-09-025-769B-25
US-09-490-070A-25
US-09-490-153-25
US-09-490-153-25
US-09-138-091A-77
US-09-138-091A-77
US-09-0330-613A-17
US-10-330-613A-17
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US-09-800-729-145
US-10-330-613A-5
US-09-343-698-6
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US-10-330-613A-9
US-09-471-276-837
                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-025-769B-39
                                                                                                                                                                                                                                                          572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      - protein search, using sw model
                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 200000000
                                                                                                                                                        US-10-735-916A-83
625
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Match Length
                            Copyright
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Perfect score:
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Minimum DB Maximum DB

Searched:

Database :

Result

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Gaps

4

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GENERAL INFORMATION:
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                          9
                                                      QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
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                          QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 510; DB 2; Length 119;
Pred. No. 2.8e-43;
3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FBB-1998
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FBB-1998
PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: MORPHO/5
TELECOMUNICATION INFORMATION:

TELECOMUNICATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:

LENGHH. 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \rm E:\ James\ F.\ Haley,\ Jr.,\ Esq.\ c/o\ Fish\ \&\ Neave1251\ Avenue\ of\ the\ Americas
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rnappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Go, Liming
APPLICANT: Go, Liming
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/ (Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 Sequence 65, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.6%;
85.0%;
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Best Local Similarity 85.0°
Matches 102, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                            US-09-025-769B-65
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US-09-490-070A-39 ; Sequence 39, Application US/09490070A ; Patent No. 6696248

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61 KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Gaps
                                                                                                                                                                                                                                                                                                                                Ge, Liming
Moroney, Simon
Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: Colin G. Sandercock, Egg. c/o Heller Ehrman
                                                                                                                                              CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Bhrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 119;
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                                                                          Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.6%; Score 510; DB 2;
85.0%; Pred. No. 2.8e-43;
tive 3; Mismatches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 65, Application US/09490070A Patent No. 6696248 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELEFAX: (202) 912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
APPLICANT: Knappik, Achim
Pack, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                   , Peter
                                                       Ge, Liming
                                                                                                                                                                                                                          CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.0
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-490-070A-65
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NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
FILING DATE: 24-Jan-2000 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.6%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10021
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-09-490-153-65
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 NPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYXCARWGGDGFYAMDYWGQGTLVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVXPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGXIXYSGSTNY 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSES: James P. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Indels
                           STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/ABENT INFORMATION:
NAME: Colin G. Sandercock, Eeq.
REGISTRATION NUMBER: 31,298
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 510; DB 2;
Pred. No. 2.8e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
      White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39, Application US/09490153
Patent No. 6706494
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
                                                                                                        ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.6%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: USA
                                              CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.0
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10021
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61 KPSLKDRVTISVDTSKNOPSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 65, Application US/09490153
; Sequence 65, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Knappik, Achim
; Ilag, Vic.
Ge, Liming
Moroney, Simon
; Housekthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Indels
FILING DATE: 18-FEB-1998
FILING DATE: 18-FEB-1998
FILING DATE: 18-FEB-1998
FILING DATE: 18-MIG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr. Bsq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 510; DB 2;
Pred. No. 2.8e-43;
3; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FRB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq.
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
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USA
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                                                                                                                                                                                                                                                                                                               RESULT 8
US-09-490-324-65
US-09-490-324-39
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                                                                                                                                                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVXPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                   KPSLKDRVTISVDTSKNOPSLKLSSVTAADTAVYYCARYGRVFF---DYWGOGTLVTVSS
                                                                                                                                                                                                                                                                                           4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
                                                                                                                                                                                                                                                  Length 119;
                                                                                                                                                                                                                                                Score 510; DB 2; Length 11
Pred. No. 2.8e-43;
3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
G, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION' Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-NUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., ESQ.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acide
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                      INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                   TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 39, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.0%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-490-324-39
                                                                                                                                                                                                         US-09-490-153-65
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61 KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
                                                                                                                                                                                                                      60 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119
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                                                                                                                                           59
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                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
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                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

CORRENT AFFICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-AUG-1995

FILING DATE: 18-AUG-1995
                                                 4,
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  Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.6%; Score 510; DB 2; Length 119;
85.0%; Pred. No. 2.8e-43;
ive 3; Mismatches 11; Indels
                                                 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
Score 510; DB 2;
Pred. No. 2.8e-43;
3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-324-65
                                                                                                                                                                                                                                                                                                                                                        Sequence 65, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Knappik, Achim
Pack, Peter
  81.6%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.0
Matches 102; Conservative
Query Match
Best Local Similarity 85.0
Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
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61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGD-GFDYWGQGTLVTVSS 117

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APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.0
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-490-070A-25
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                                                                           RESULT 11
US-09-025-769B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
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60 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 OVOLOESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGLEWIGSIYHSGSTYY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARGKWSKFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 81.1%; Score 507; DB 2; Length 117; Best Local Similarity 84.6%; Pred. No. 5.5e-43; Matches 99; Conservative 2; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
79.5%; Score 497; DB 2; Length 117;
Best Local Similarity 84.7%; Pred. No. 5.4e-42;
Matches 100; Conservative 3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-330-6134-13

Sequence 13, Application US/10330613A

Sequence 13, Application US/10330613A

Fatent No. 6924360

GENERAL INFORMATION:

APPLICANT: Gudas, Jean

TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN

FILE REFERENCE: ABGENIX.022A

CURRENT APPLICATION NUMBER: US/10/330,613A

CURRENT FILING DATE: 2002-12-26

PRIOR APPLICATION NUMBER: 60/346299

PRIOR PILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 90

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                        APPLICANT: Williams, Andrew J
APPLICANT: Tempest, Philip R
APPLICANT: Tempest, Philip R
APPLICANT: Holtet, Thor L
APPLICANT: Holtet, Thor L
APPLICANT: Holten
APPLICANT: Daramola Holen
APPLICANT: Daramola Olalekan
APPLICANT: Daramola Olalekan
APPLICANT: Daramola Olalekan
APPLICANT: Daramola Olalekan
APPLICANTON: Improvements relating to antibodies
FILE REPERENCE: AHB/CP5775333
CURRENT FILING DATE: 2002-10-23
FRIOR APPLICATION NUMBER: GB 9814383.7
PRIOR FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
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Patent No. 6827925
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology Limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-330-613A-13
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LENGTH: 117
                                                                                                                            US-09-720-493-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 117
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1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGEIYHSGSTNY 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OVOLOESGPGLUKPSETLSLTCTVSGYSISGGYLWNWIROPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT PAPPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F: Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REPREMENCE/DOCKET NUMBER: MORPHO/5
TELEPHONE: (212)596-9000
TELEPHONE: (212)596-9000
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Indels
                                                                                                                                                                                                                                                                                                              ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
                                                                          APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plucekthum, Andreas
APPLICANT: Plucekthum, Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 493.5; DB 2
Pred. No. 1.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
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Sequence 25, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
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84.0%;
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RESULT 14
US-09-490-324-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCA -- RYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGRGGGGVFDYWGQGTLVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                      COUNTRY: UCHT

ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: DEADEN: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.30 (BPO)
SOFTWARE: Petentin Release #1.0, Version #1.30 (BPO)
SOFTWARE: Petentin NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTER: 2020
TELECOMMUNICATION OF 25:
SEQUENCE CHARACTER: 51CS:
LENGTH: 118 amino acids
                                                                      ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                       STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 79.0%; Score 493.5; DB 2
Best Local Similarity 84.0%; Pred. No. 1.2e-41;
Matches 100; Conservative 3; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
                                                                                                                                             CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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US-09-490-153-25
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1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGEIYHSGSTNY 59
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Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRUPTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DoS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
                                                        Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 118;
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                                                                                                                                                                          APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
FILING DATE: 18-FEB-1998
FILING DATE: 18-MC-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Bsq.
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELEPHONE: (212) 596-9090
INFORMATION FOR SEQ 1D NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.0%; Score 493.5; DB 2
84.0%; Pred. No. 1.2e-41;
tive 3; Mismatches 13
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURENT APPLICATION DATA:
APPLICATION WUMBER: US/09/490,153 FILING DATE: 24-Jan-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/09490324; Patent No. 6828422; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 100; Conservative
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STATE: New York
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGEIYHSGSTNY 59
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78.8%; Score 492.5; DB 2; Length 244;
Best Local Similarity 83.8%; Pred. No. 3.7e-41;
Matches 98; Conservative 7; Mismatches 9; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Pest Local Similarity 84.0%; Pred. No. 1.2e-41;
Matches 100; Conservative 3; Mismatches 13; Indels 3
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRATION INFORMATION:
FELEPONE: (212)596-9000
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
FTYPE: amino acids
FTYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19. Application US/08918148A
Patent No. 634220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Gerter, Paul J.
APPLICANT: APPLICATION NUMBER: US/08/918,148A
CURRENT PILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
ILENGTH: 244
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
US-08-918-148-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-08-918-148-79
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Search completed: January 10, 2006, 20:58:05 Job time: 22.847 secs

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2006
           Copyright
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- protein search, using sw model OM protein

January 10, 2006, 20:07:41; Search time 80.7649 Seconds (without alignments) 636.505 Million cell updates/sec Run on:

US-10-735-916A-83 625 Title: Perfect score:

1 QVQLQESGPGLVKPSETLSL.....RYGRVFFDYWGQGTLVTVSS 117 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 seqs, 439378781 residues Searched:

Total number of hits satisfying chosen parameters:

2443163

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

geneseq1980s:* geneseq2000s:* geneseq2000s:* geneseq2001s:* geneseq2002s:* geneseq2003s:* geneseq2003s:* geneseq2004s:* A_Geneseq_21:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Adj76917 Anti-IGF-	Adz67087 Human ant	Adj76919 Anti-IGF-	Adz67089 Human ant	Adj76913 Anti-IGF-	Adz67083 Human ant	Adj76915 Anti-IGF-	Adz67085 Human ant	Adj76909 Anti-IGF-	Adz67079 Human ant	Adj76911 Anti-IGF-		Adj76903 Anti-IGF-	Adz67073 Murine im	Adj76886 Anti-IGF-	Adz67056 Murine im	Aay15126 Anti-muri	Adp03973 Murine-ex	Ads16559 Human ant	Adc27457 Humanised	Adp03885 Murine-ex	Adp03889 Murine-ex	Adp03958 Murine-ex	Adp03957 Murine-ex
SOMMAKIES	ΩΙ	ADJ76917	ADZ67087	ADJ76919	ADZ67089	ADJ76913	ADZ67083	ADJ76915	ADZ67085	ADJ76909	ADZ67079	ADJ76911	ADZ67081	ADJ76903	ADZ67073	ADJ76886	ADZ67056	AAY15126	ADP03973	ADS16559	ADC27457	ADP03885	ADP03889	ADP03958	ADP03957
	Length DB	117 7	117 9	135 7	135 9	117 7	117 9	135 7	135 9	117 7	117 9	135 7	135 9	117 7	117 9	127 7	127 9	246 3	119 7	121 8	120 7	122 7	122 7	120 7	116 7
de	Query Match I	100.0	100.0	100.0	100.0	98.4	98.4	98.4	98.4	97.8	97.8	97.8	97.8	84.6	84.6	84.6	84.6	83.1	82.7	82.6	82.3	82.2	82.2	82.0	81.7
	Score	625	625	625	625	615	615	615	615	611	611	611	611	529	529	529	529	519.5	517	516.5	514.5	513.5	513.5	512.5	510.5
	Result No.		8	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Abb07171 ebvHigM M Adi26658 Human ant Adp03887 Murine-ex Adp03884 Murine-ex Aaw27554 Human Ab Abj18676 Antibody Ady1798 Human IgG		Human Human Human Human Human	Ade28471 Human ant Adx01828 SARS coro Adp03870 Murine-ex Adx01838 SARS coro
ABB07171 AD126658 ADP03887 ADP03884 AAW27554 ABJ18676 ABJ18676	AA144615 ADE28455 ADE28479 AA030915 AA030913	AKAZ1456 ADX98267 ADS16505 ADS16613 ADE28491	ADE28471 ADX01828 ADP03870 ADX01838
1121 1121 1122 1122 1119 1119 1119 1119	21 21 2 21 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3	22392	21 9 7 23 7 48 9
510.5 510.5 510.5 510.5 510.5 510.5 510 510 510 510 510 510 510 510 510 51	88 88 11 11 11 11 11 11 11 11 11 11 11 1	88888 80.98 80.7.09	
25 27 27 28 29 30 31 31	አ ፡፡ ፡፡ ፡፡ ፡፡ ፡፡ ፡፡ ፡፡ ፡፡ ፡፡ ፡፡ ፡፡ ፡፡ ፡፡	2.0 2.0 2.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3	4 4 4 4 5 6 4 8

ALIGNMENTS

cytostatic; antipsoriatic; antibody; idf-1R; tyrosine kinase activity; insulin-11ke growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosaccoma; complementarity determining region; ADJ76917 standard; protein; 117 AA Anti-IGF-1R related protein #26. 06-MAY-2004 (first entry) ADJ76917; ADJ76917

Homo sapiens.

WO2003059951-A2.

24-JUL-2003.

20-JAN-2003; 2003WO-FR000178.

18-JAN-2002; 2002FR-00000653. 18-JAN-2002; 2002FR-00000654. 07-MAY-2002; 2002FR-00005753.

(FABR) FABRE MEDICAMENT SA PIERRE. Leger O; Corvaia N, Goetsch L,

WPI; 2003-569653/53.

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

Disclosure; SEQ ID NO 83; 164pp; French

οĘ The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (IGFR) and/or epidermal growth factor receptor (IGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of

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             transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                    KPSLKDRVTISVDTSKNOPSLKLSSVTAADTAVYYCARYGRVFFDYWGOGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                     KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                  QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human antibody 7C10 3 heavy chain variable region SEQ ID NO:83.
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                                                                                                                                                                    Length 117;
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receptors with their ligands. Especially they inhibit
                                                                                                                                                                                                 Indels
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                                                                                                                                                                100.0%; Score 625; DB 7;
100.0%; Pred. No. 1.9e-49;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duflos A,
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                                                                                                                                                                                                                                                                                                                                                                                                                    ADZ67087 standard; protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
20-JANY-2003; 2003FR-0000178.
11-JUL-2003; 2003FR-00006538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-DEC-2003; 2003US-00735916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                   Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goetsch L, Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-321968/33
                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DUFLOS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAEUW J.
                                                                                                                                   Sequence 117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADZ67087;
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(LEGE/)
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(HAEU/)
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The invention relates to a novel isolated anti-insulin-like growth ractor capable of binding to human IGF-IR and, if necessary, capable of spable of spable of binding to human IGF-IR and, if necessary, capable of spable of spable of binding to human IGF-IR and, if necessary, capable of spable of spable of spable of spable of the invention is useful in comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary cardet ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or connected with a broomal activation of the IGF-IR and/or EGFR, and/or connected with a horizon of the medicament does not induce or only slightly interaction of IGFI or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly creeppor. The antibody is useful for preparation of a medicament intended to inhibit the growth caparation of a medicament intended to inhibit the growth and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent calls. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of psoriadis. (I) is useful in the preparation of a medicament intended for prevention or colon cancer. (I) is useful in preparation of a medicament intended for the prevention or for the preparation of a medicament intended for the prevention or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or colon cancer. (I) is useful in
a novel isolated anti-insulin-like growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGXISYDGTNNY
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100.0%; Pred. No. 1.9e-49;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 117 AA;
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or reat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate. Jung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 85; 164pp; French.
                                                                                                                                                                                                                                                                                   (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                      18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
                                                                                                                                                                                                                                                                                                                                                                                        Corvaia N,
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                                                                                                                                                                61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                 1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                         Gaps
                                       .
0
100.0%; Score 625; DB 7; Length 135; 100.0%; Pred. No. 2.2e-49; tive 0; Mismatches 0; Indels (
                Best Local Similarity 100.
Matches 117; Conservative
    Query Match
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Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipporiatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                        Human antibody 7C10 3 heavy chain variable region SEQ ID NO:85
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
           ADZ67089 standard; protein; 135 AA.
                                                                            (first entry)
                                                                                                                                                                                                                                                                        Homo sapiens
                                                                          30-JUN-2005
ADZ67089
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Sequence 135 AA;

/note= "leader peptide"

Peptide Region

/note= "CDR1"

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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting to human IGF-IR and, if necessary, capable of specifically inhibiting to have a civily of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in a determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in a illness connected with an overexpression and/or a butormal activation of the IGF-IR and/or EGFR, and/or connected with a ctivation of the IGF-IR and/or EGFR, and/or connected with an abnormal activation of the IGF-IR and/or EGFR, and/or connected with and activation of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin creceptor. The antibody is useful for preparation of a medicament intended contacter, preferably IGF-dependent and/or IREZ/neu-dependent calls. (I) is useful in the capacity of the proparation of a medicament intended for prevention or tor the treatment of cancer, on undor the proliferation of the medicament of cancer. (I) is useful in the preparation of a medicament of percention of a medicament of percention or coll con cancer. (I) is useful in the preparation of a medicament of percention or coll con cancer. (I) is useful in the preparation of a medicament of percention of undometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the specific targeting of a biologically active compound to call supplied for in vitro diagnosis of illnesses induced by an expensing or an underexpression or an underexpression of the IGF-IR and/or EGFR receptor. If is useful in the exemplification of the invention of the inventio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duflos A, Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 13; SEQ ID NO 85; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leger O,
69. .84
/note= "CDR2"
                                   117. .124
/note= "CDR3"
                                                                                                                                                                                                                           18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                   16-DEC-2003; 2003US-00735916
                                                                                                                                                                                                       2002FR-00000653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corvaia N,
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                                                                                                                                                                                                                                                                                                                         GOETSCH L. CORVAIA N.
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                                                                                           US2005084906-A1
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                                                                                                                                 21-APR-2005.
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or creat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells, nour cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                              78
                                                                                                                                                   KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                        KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibodies that bind to human insulin-like growth factor receptor, ful for treatment, prevention and diagnosis of cancers.
                                                                                                 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                          Gaps
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0
 Length 135;
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Pred. No. 1.6e-48;
1; Mismatches 1; Indels
                                      Indels
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; Score 625; DB 9;
; Pred. No. 2.2e-49;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; antipsoriatic; antibody;
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                                                                                                                                                                                                                                                                               ADJ76913 standard; protein; 117
                                                                                                                                                                                                                                                                                                                                                                                          Anti-IGF-1R related protein #24.
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   100.0%;
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07-MAY-2002; 2002FR-00005753.
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Best Local Similarity 98.3%;
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                      117; Conservative
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   Query Match
Best Local Similarity
Matches 117; Conserv
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, Gapable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADSCF006 and ADZCF014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a activation of the transduction pathway of the signal mediated by the interaction of IGFP IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly
                                                                                                                                                                                                                                                                                                          Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lump tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
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                                                             KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                KPSLKDRVIISRDISKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGGGTLVIVSS 117
               Human antibody 7C10 2 heavy chain variable region SEQ ID NO:79.
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                                                                                                                                                                              ADZ67083 standard; protein; 117
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2002FR-00005753.
2003WO-FR000178.
2003FR-00008538.
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                                                                                                                                                                                                                                                                                                                                                                                                             heavy chain variable region
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CORVAIA N.
LEGER O.
DUFLOS A.
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BECK A.
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11-JUL-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HAEU/)
(BECK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GOET/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORV/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DOFL)
                                                                                                                                             RESULT 6
ADZ67083
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induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2.

Gependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful for preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent.

CHER2/neu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the prevention of a medicament intended for the prevention of cancer compound to cells expressing or overexpressing the IGF-IR and/or EGPR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                            overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibodies that bind to human insulin-like growth factor receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 615; DB 9;
Pred. No. 1.6e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ76915 standard; protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-IGF-1R related protein #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leger 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JAN-2003; 2003WO-FR000178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.3%;
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-569653/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003059951-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goetsch L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ76915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ76915
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fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or spidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, no are useful against cancers of the profiterate. Iung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abuncarial expression of IGF-IR and/or EGFR. This sequence represents a beautiful and the superior of the profit of the profits of IGF-IR and/or EGFR. This sequence represents a beautiful and the sequence represents a beautiful and the sequence represents a profit of the profits 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostette tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriasis; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPSLKDRVTISVDISKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human antibody 7C10 2 heavy chain variable region SEQ ID NO:81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 615; DB 7; Length 135;
Pred. No. 1.8e-48;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         protein sequence used to generate the Ab of the invention.
useful for treatment, prevention and diagnosis of cancers.
                                                                                               (Ab)
                                                                                               invention relates to an isolated antibody
                                                 Disclosure; SEQ ID NO 81; 164pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .. .18
'note= "leader peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADZ67085 standard; protein; 135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .54
-- "CDR1"
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/note= "CDR2"
117. .124
/note= "CDR3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2005084906-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
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ADJ76909 standard; protein; 117 AA.

RESULT 9 ADJ76909 Anti-IGF-1R related protein #22.

(first entry)

06-MAY-2004

ADJ76909;

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I receptor (IGP-IR) antibody (I) or its functional fragment, being capable of binding to human IGP-IR and, if necessary, capable of apable of binding to human IGP-IR and, if necessary, capable of pecifically inhibiting tyroshae kinase activity of the receptor, capable of pecifically inhibiting tyroshae kinase activity of the receptor, comprising a light or heavy chain having at least one complementary cardetermining region (CDR) consisting of one of two fully defined is amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an intended of the IGP-IR and/or connected with a crivation of the IGP-IR and/or EGPR, and/or connected with a cativation of the IGP-IR and/or EGPR, and/or connected with intended connected with inhibition of the insulin receptor. The antibody is useful for preparation of the medicament intended connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended connected with inhibition of the insulin caparation of a medicament intended to inhibit the growth and/or the proliferation of twent canels. Where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention of the preparation of a medicament of portable (I) is useful in preparation of a medicament of prevention or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention of a medicament of portable in which the abnormal presence, of IGP-calcal for in vitro diagnosis of illnesses induced by an experience of Insancer of In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 615; DB 9;
Pred. No. 1.8e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; SEQ ID NO 81; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leger O,
                                 20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goetsch L, Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-321968/33.
                                                                                                                                                          GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                DUFLOS A. HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADZ67084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                   BECK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                (DUFL/)
(HAEU/)
(BECK/)
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                                                                                                                       19 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                0; Gaps
                                                1; Indels
98.3%; Pred. No. 1...
98.3%; Pred. No. 1...
1; Mismatches
                            Best Local Similarity 98.3
Matches 115; Conservative
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RESULT 10

ADZ67079

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or reat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of transformation of tumor cells, so are useful against cancers of the profileration of tumor cells, so are useful against cancers of the profileration of tumor cells, and only, also osteosarcoma, and also for treating psoriaais. Ab are a lso used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                    cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein sequence used to generate the Ab of the invention
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 75; 164pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (FABR ) FABRE MEDICAMENT SA PIERRE.
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18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                                                                                                 20-JAN-2003; 2003WO-FR000178.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-569653/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 117 AA;
                                                                                                                                                                                                                                                         WO2003059951-A2.
                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                             24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goetsch L,
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The invention relates to a novel isolated anti-insuli. Like growth ractor capable of binding to human IGP-IR and, if necessary, capable of capable of binding to human IGP-IR and, if necessary, capable of specifically inhibiting tyroshine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGP-IR and/or EGFR, and/or connected with a cativation of the IGP-IR and/or of EGFR, where interaction of the IGP-IR and/or of EGFR, where interaction of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin contained in the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2.

CC receptor. The antibody is useful for preparation of a medicament intended to inhibit the growth contained in the proparation of a medicament intended to inhibit the growth cuseful for preparation of a medicament intended to inhibit the growth and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent of a medicament intended for prevention or for the treatment of cancer, where the ERZ/neu-dependent cells. If is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer. (I) is useful in the
                                                                                                                                                        Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; reoplasm; prosteate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gymecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated anti-insulin-like growth factor
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                                                                                                                    Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 13; SEQ ID NO 75; 125pp; English.
ADZ67079 standard; protein; 117 AA
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2002FR-00005753.
2003WO-FR000178.
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                                                                            (first entry)
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CORVAIA N.
LEGER O.
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20-JAN-2003;
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                                                                              30-JUN-2005
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(LEGE/)
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(HABU/)
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preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR.
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                                                                                                                                                                                                                                                                                                                                                                                     61 KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 3.7e-48;
3; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; antipsoriatic; antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ76911 standard; protein; 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-IGF-1R related protein #23.
                                                                                                                                                                                                                                        97.8%;
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07-MAY-2002; 2002FR-00005753
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Aatches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-569653/53
                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                         Sequence 117 AA;
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Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                      N-PSDB; ADZ67080
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       transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast; endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                   neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; andocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
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                                                                                                                                                                                          KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                        KPSLKDRITISRDISKNQFSLKLSSVTAADIAVYYCARYGRVFFDYWGQGTLVTVSS 135
                                                                                                                                                 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                    Human antibody 7C10 1 heavy chain variable region SEQ ID NO:77.
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receptors with their ligands. Especially they inhibit
                                                                                                        Length 135;
                                                                                                                             1; Indels
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                                                                                                         Score 611; DB 7;
Pred. No. 4.3e-48;
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                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "leader peptide"
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/note= "CDR2"
117. .124
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/note= "CDR1"
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'note= "CDR3"
                                                                                                        97.8%;
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2002FR-00005753
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                                                                                                                             Matches 113; Conservative
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                                                                                                      Query Match
Best Local Similarity
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CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DUFLOS A.
                                                                                   Sequence 135 AA;
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                                                                                                                                                                      13
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                                                                                                                                                                                                                                                                                           ADZ67081;
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(HABU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BECK/)
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Traceptor (IGF-IR) antibody (I) or its functional fragment, being capable of capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tryosine kinase activity of the erceptor, comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary cardes (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a crivation of the IGF-IR and/or EGFR, and/or connected with a chinistration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral caparation of a medicament intended to inhibit the growth and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent cells, preferably IGF-dependent of more cells, preferably IGF-dependent cells, in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, capacital cancer, capacital or and cancer, in intended for prevention or for the preparation of a medicament intended for the prevention or for the creatment of psoriadis. (I) is useful in preparation of a medicament intended for the prevention or core colls expressation or a medicament intended for the prevention or core colls expressing or overexpressing the IGF-IR and/or EGFR receptor. It suseful for in virco diagnosis of illnesses induced by an or cel
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                                                                                   The invention relates to a novel isolated anti-insulin-like growth
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Pred. No. 4.3e-48;
3; Mismatches 1; Indels
Example 13; SEQ ID NO 77; 125pp; English.
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96.6%;
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Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (IGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis, Ab are a slo used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VQLQBSGPGLVKPSETLSLTCTVSGYSISGGYLMNWIRQPPGKGLEWIGYISYDGTNNYK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VOLQESGPGLVKPSQSLSLTCSVTGYSITGGYLMNWIRQFPGNKLEWMGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 PSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 PSLKDRISITRDTSKNOFFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.6%; Score 529; DB 7; Length 11
82.8%; Pred. No. 1.2e-40;
ive 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 69; 164pp; French
                                                                                                                                                                                                                                                                                                                                            (FABR ) FABRE MEDICAMENT SA PIERRE.
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                                                                                                                                                                                                                                                                                                                                                                                    Leger 0;
                                                                                                                                                                                                                                                              18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                        20-JAN-2003; 2003WO-FR000178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 82.8%
hes 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-569653/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 117 AA;
                                                                                                                                        WO2003059951-A2
                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2005
                                                                                                                                                                                24-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADZ67073;
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and; if necessary, capable of specifically inhibiting to have a capable of specifically inhibiting the way chain having a light or heavy chain having a least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67014). An antibody of the invention is useful in a cids (ADZ67016 and ADZ67014). An antibody of the invention is useful in a lineas connected with an overexpression and/or a banormal activation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or a banormal activation of the IGF-IR and/or EGFR, and/or connected with an abnormal activation of the IGF2014 In Intended of EGF with EGFR, where interaction of IGF2014 In Intended or EGF with EGFR, where interaction of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulant receptor. The antibody is useful for preparation of a medicament intended contacter, preferably IGF-dependent, especially IGF1 and/or IGF2-dependent and/or EGF-dependent cells (I) is useful in the preparation of a medicament intended for prevention or too the preparation of a medicament intended for prevention or ancer. (I) is useful in the preparation of a medicament intended for the prevention or ancer, endometrial cancer or colon cancer. (I) is useful in the experience of a underexpression or an underexpression or an underexpression or an underexpression or an endometrial sample with involves contacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 13; SEQ ID NO 69; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leger 0,
                                                                                                                                                                                                                                                       2002FR-00000654.
2002FR-00005753.
2003WO-FR000178.
                                                                                                                                                                                                16-DEC-2003; 2003US-00735916
                                                                                                                                                                                                                                     2002FR-00000653
                                                                                                                                                                                                                                                                                                                11-JUL-2003; 2003FR-00008538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for treating cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-321968/33.
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CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                 DUFLOS A. HAEUW J.
                                                                                                                  US2005084906-A1.
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                                                                               Mus musculus.
                                                                                                                                                                                                                                                                          07-MAY-2002;
20-JAN-2003;
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(HAEU/)
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Sequence 117 AA;

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (1) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (1i) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or pidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit growth and/or proliferation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating pseciasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                 VOLOESGPGLVKPSOSLSLTCSVTGYSITGGYLMNWIROFPGNKLEWMGYLSYDGTNNYK
                                                                         2 VOLORSGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK
                                                                                                                                                                         PSLKDRVTISVDTSKNOPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                        Gaps
                                        ö
   Length 117;
                                      9; Indels
Match 84.6%; Score 529; DB 9; Local Similarity 82.8%; Pred. No. 1.2e-40; les 96; Conservative 11; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 52; 164pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                    ADJ76886 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leger O;
                                                                                                                                                                                                                                                                                                                                                                                                   Anti-IGF-1R related protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JAN-2002; 2002FR-0000653.
18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-0005753.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                              06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUL-2003.
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 Query Match
                                      Matches
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Length 127;

Score 529; DB 7; Pred. No. 1.3e-40;

84.6%;

Query Match Best Local Similarity

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                                                          12 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK 71
                               2 VQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK
                                                                                               PSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                72 PSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 127
 Gaps
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9; Indels
 11; Mismatches
 96; Conservative
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   Matches
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Search completed: January 10, 2006, 20:44:18 Job time : 81.7649 secs

5.1.6 Compugen Ltd. GenCore version (c) 1993 - 2006 Copyright

- protein search, using sw model OM protein January 10, 2006, 20:28:02; Search time 14.1157 Seconds (without alignments) 797.508 Million cell updates/sec Run on:

US-10-735-916A-83 625 1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Ig variable region	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain - h	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain - h	Ig heavy chain pre	Ig heavy chain pre	c	Ig heavy chain V r	Ig heavy chain V r	c	¤	¤	G	Ig heavy chain V r	hypothetical hybri	Ig heavy chain pre	heavy chain	heavy	heavy chain V	heavy chain V	heavy c	ret.	heavy	
ΩI	137782	S31690	830530	813519	831511	S24443	S30534	S31586	831512	S78052	S78055	844113	S44114	A49045	S78051	S31676	809711	S47010	S20780	A24770	A26340	809710	S12421	S31696	837200	S26906	844125	S30529	S54906
Length DB		130 2			155 2	118 2	0	σ.	155 2	0			129 2		-		146 2				118 2			139 2			105 2	m	4
& Query Match		90.6	78.6	ω.	76.5	75.8	ď.	L)	75.5	75.4	75.1	74.7	74.6	74.6	74.4	74.0	73.9	73.7	73.2		71.9			711.7	71.4	71.1			71.0
Score	519	504	491	488	478	473.5	473.5	473.5	472	471.5	469.5	467	466.5	466	465	462.5	462	460.5	457.5	456	449.5	449	448	448	446	444.5	444.5	444	444
Result No.	-1	7	٣	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Ig heavy chain pre Ig heavy chain V r	ig heavy chain v r ig heavy chain v r ig heavy chain v r ig V-D-J region (N ig heavy chain pre
B26340 S07637 S26902 S19668 S19668 S12416 S38718 S26802 B49028 S37456	128195 831514 826801 869912 A41287
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116 136 137 137 116 116 199 1143	117 128 122 139
71.0 70.9 70.9 70.6 70.6 70.3	69.8 69.8 69.8 69.8
444 4444 444 444 444 444 444 444 444 4	438 436.5 436.5 436.5
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## ALIGNMENTS

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		human	
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		T23-9)	
		(clone	(878)
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		region	Homo con
RESULT 1	137782	Ig variable region (VDJ) (clone T23-9)	(man) ordings conjugated
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C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: 137782; S25476
C;Accession: 137782
R;Demaison, C.; Chastegner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by i A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: 137782
A;Status: preliminary

A; Molecule type: mRNA

A;Residues: 1-140 <RES>
A;Cross-references: UNIPARC:UPI0000176E83; EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PI: C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;46-128/Domain: immunoglobulin homology <IMM>

Gaps 8 Query Match 83.0%; Score 519; DB 2; Length 140; Best Local Similarity 84.6%; Pred. No. 5.7e-40; Matches 104; Conservative 3; Mismatches 8; Indels

9 78 20 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY 1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 요 ઠ

61 KPSLKDRVTISVDISKNQFSLKLSSVTAADTAVYYCAR-----YGRVFFDYWGQGTLVT 114 ò

138 VSS 140 115 VSS 117 ð 셤

요

Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31690
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585
A;Accession: S31690

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <CUT.>
A;Cross-references: UNIPARC:UPI0000116471; EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PI:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

us-10-735-916a-83.rpr

Length 147;

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Ig heavy chain V region (VH4DJ) - human
78.1%;
81.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.5%;
78.2%;
                                        99; Conservative
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Matches 97; Conserv
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C;Date: 22-Jan-1993 #seç
                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain - human
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(c.species: Homo sapiens (man)

(c.species: Mark)

(c.species: Mark)

(c.species: Mark)

(c.species: Mark)

(d.species: Homologlobulin V region; immunoglobulin homology

(d.species: Homologlobulin Nomology < Nomology
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                                                                                                                                                                                                                           KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRV-----FFDYWGQGTLV 113
                                                                                                                                             6 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYMSMSRQPPGKGLEWIGYIYYSGSTNY 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                             C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C. Accession: S30530
A. Raitete, X.
Submitted to the EMBL Data Library, October 1992
A. Reference number: S30520
A. Reference number: S30530
A. Status: preliminary
A. Rolecule Cype: mRNA
A. Residues: 1-123 *AAAA>
A. Residues: 1-123 *AAAA>
Cross-references: UNIPARC:UPI0000176C83; EMBL:Z18316
C. Superfamily: immunoglobulin V region; immunoglobulin homology
C. Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IPM>
                                                                                                                                                                                                      61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-----YGRV--FFDYWGQGT
                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                  Gaps
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                                                                                  10;
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                                          Length 130;
                                                                                10; Indels
                                        Score 504; DB 2;
Pred. No. 1.2e-38;
5; Mismatches 10
F;20-102/Domain: immunoglobulin homology <IMM>
                                        Query Match 80.6%;
Best Local Similarity 80.2%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               heavy chain V region - human
                                                                                                                                                                                                                                                                                    LVTVSS 117
                                                                                                                                                                                                                                                                                                                            LVTVSS 130
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Best Local Similarity
Matches 98; Conserv
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31511
R;Chastagner, P:; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Actus: mRNA
A;Molecule type: mRNA
A;Residues: 1-155 <CHLA>
A;Cross-references: UNIPARC:UP100001160FF; EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PIC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mENA
A;Residues: 1-118 JUN>
A;Residues: 1-118 JUN>
A;Cesidues: Lebences: UNIPARC:UPI0000115FE9; EMBL:X61650; NID:g37720; PIDN:CAA43831.1; PII
B;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRV--FFDY-----WGQGTLV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 NPPLKSRVTISVDISKNQFSLKVSSVTAADTAVYYCARGGGISSWYDYYGMDVWGQGTTV 151
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                                                                                                                                                                          27 QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTY
                                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGYSI-SGGYLWNWIRQPPGKGLEWIGYISYDGTNN
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                                                                  Indels
                                                                     13;
Score 488; DB 2;
Pred. No. 3.8e-37;
4; Mismatches 13
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Pred. No. 3.2e-36;
6; Mismatches 13;
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R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
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A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
                                                                                                                                                                                   116
                                                                                                                                                                                                      79 NPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARGGLGIRRGAFDIWGGGTMVTVS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVF-----FDYWGQGTLV 113
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C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78052; S23717
R;Harindranath, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
                                                                                                           20 QVQLQESGFGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPAGKGLEWIGRIYTSGSTNY
                                                                                                                                                                                      61 KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYG----RVFFDYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIXYTGSATX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                             1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                           Indels
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A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23717
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  7.3e-36;
thes 15;
Pred. No. 7.3e-
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A;Reference number: S78051
A;Accession: S78052
A;Molecule type: mRNA
A;Residues: 1-140 <HAR>
        80.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 76.6
Matches 95; Conservative
                              97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S31509
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     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-155 <CHA>
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Matches
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S1586
Ig heavy chain V region - human (fragment)
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31586
E;Cuisinier, A.m.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A;Pescription: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31586
C;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <CUI>A;Cross-references: UNIPARC:UPIO00011646E; EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PIC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region - human
C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30534
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Reference number: S30520
A;Accession: S30534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 < MAR>
A;Cross-references: UNIPARC:UPI0000113P45; EMBL:218320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hereroterramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <INM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YNPSIKSRVTISVDTSKNQFSIKLSSVYTAADTAVYYCARDKGGFWSGYYTRNSRAAFDIW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
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                                                                                                                                                                                                                                                                                                                                                                                    60 NSSLQSRVTISADTSKNQFSLKLSSVTAADTAVYYCARSFSNSFFFGYWGQGTLVTVSS 118
                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGYSI-SGGYLWNWIRQPPGKGLEWIGYISYDGTNN
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                                                                                                                                                                                           3,
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                                                                                                                                          Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 130;
                              C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                       Score 473.5; DB 2;
Pred. No. 6.1e-36;
5; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
        A;Cross-references: UNIPARC:UPI0000176B52; EMBL:X61650
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                                                                                                                                       Query Match 75.8%;
Best Local Similarity 79.8%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 74.6'
Matches 97; Conservative
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GQGTMVTVSS 130
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Query Match

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13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
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       C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
hes 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <HAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 TVSS 117
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CyBecies: Homo sapiens (man)
CyBecies: Homo sapiens (man)
CyBecies: Homov-1997 #text_change 23-Jul-1999
CyAccession: S78055; 823720
R;Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78055
A;Accession: S78055
A;Residues: 1-145 c+HAR.
A;Residues: 1-145 c+HAR.
A;Cross-references: UNIPARC:UPIO000115E8C; EMBL:X54445; NID:g37817; PIDN:CAA38312.1; PIL
R;Harindranath, N.; Goldfarb, I.S.; Ikemateu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Harindranath, N.; Goldfarb, I.S.; Ikemateu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Harindranath, N.; Accession: S23716; MUID:92031262; PMID:1718404
A;Accession: S2370
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S2370
A;Residues: 18-115 c+HAW.
A;Residues: immunoglobulin V region; immunoglobulin homology
C;Gywords: immunoglobulin (fragment) #status predicted cSIG.
F;18-145/Product: 1g haavy chain (fragment) #status predicted cAIG.
F;18-145/Product: 1g haavy chain (fragment) #status predicted cAIG.
F;32-115/Domain: immunoglobulin homology cIMM.
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                                                                                                                                                                                                                                                                                                                                                                                    KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVF------FDYWGQG 110
                                                                                                                                                                                                                                                                                                                                                                                                                 61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-----YGR-VFFDYWGQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                              15 QVQLQQWGAGLIKPSETLSLTCAVYGGSFS-GYYWSWIRQPPGKGLEWIGEINHSGSTNY 73
                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                     11;
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A;Cross-references: UNIPARC:UPI0000116417; EMBL:X54441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F;15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;29-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.1%; Score 469.5; DB 2; Length 145; 74.2%; Pred. No. 1.7e-35; ive 5; Mismatches 17; Indels 11;
                                                                                                                                                                                 DB 2; Length 140;
                                                                                                                                                                                 Query Match 75.4%; Score 471.5; DB 2; Length Best Local Similarity 74.8%; Pred. No. 1.1e-35; Matches 95; Conservative 6; Mismatches 15; Indels
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844113
Ig heavy chain V region - human
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95; Conserv
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Best Local S
Matches 95
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C;Accession: S44113
C;Accession: S44113
C;Accession: S44113
C;Accession: S.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
Submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
A;Accession: S44113
A;Accession: S44113
A;Accession: S44113
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                A;Residues: 1-121 <HAW>
A;Cross-references: UNIPRC:UPI000011662F; EMBL:Z31389; NID:g472967; PIDN:CAA83264.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Date: 13-Jan-1995 #sequence_revision 8.; Hamblin, T.J.; Stevenson, F.K.
B;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Bescription: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Accession: §44114
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F;15-98/Domain: immunoglobulin homology < IMM>
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Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C;Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.7%; Score 467; DB 2;
ilarity 76.9%; Pred. No. 2.4e-35;
Conservative 4; Mismatches 20
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C;Accession: S78051; S23716
C;Accession: S78051; S23716
Submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78051
A;Accession: S78051
A;Accession: S78051
A;Residues: 1-135 <-HAR>
A;Cross-references: UNIPARC:UP10000115E87; EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID
B;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int: Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: A49045
E;Accession: A49045
A;Reference number: A191-1788, 1992
A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes ibla, A;Reference number: A49045
A;Reference number: A49045
A;Rocession: A49045
A;Rocession: A49045
A;Rolecule type: DNA
A;Rolecule type: DNA
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C;Rolecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRV----FFDYWGQGTLVTV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
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Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
Accession: S78051; S23716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 74.4%; Score 465; DB 2; Length 135; Best Local Similarity 77.2%; Pred. No. 4.1e-35; Matches 95; Conservative 4; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.6%; Score 466; DB 2; Length 140; 77.0%; Pred. No. 3.5e-35; Live 6; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S23716
A;Molecule type: mRNA
A;Residues: 13-111 - HAMA
A;Cross-references: UNIPARC:UPI00001769D5; EMBL:X54437
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-13/Domain: signal sequence (fragment) #status predicted <SIC
F;14-135/Product: Ig heavy chain (fragment) #status predicted <AT
F;27-111/Domain: immunoglobulin homology <IMMA
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Search completed: January 10, 2006, 20:55:16 Job time : 15.1157 secs THIS PAGE BLANK (USPTO)

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                                                        January 10, 2006, 20:26:41;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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20 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-GYYWSWIRQPAGKGLEWIGRIYTSGSTNY 78

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TISSUE-Primary B-Cells;

RA INCLEOTIDE SEQUENCE.

RA Straushers R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Straushers R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Heith F.,

Rapleton M., Soares M.B., Bonaldo M.F., Carnhori P., Scheetz T.E.,

Rapleton M., Soares M.B., Bonaldo M.F., Carnhori P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Hichards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A.,

Richards A., C., Grimwood J., Schmutz J., Myers R.M.,

RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

RA Monson And initial analysis of more than 15,000 full-length human
                                                                                                            60 TPSLKSRVTISVDRSKNOFSLKITSLTAADTAVYFCARLSNWGPYYFDYWGQGTLVTVSS 119
                                                                                      61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR---YGRVFFDYWGQGTLVTVSS 117
QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
                                           59
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                               QVQLQESGPGLVKPSETLSLTCTVSGGSIC-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.0%; Score 493.5; DB 2; Length 465; 83.8%; Pred. No. 2.1e-41; ive 4; Mismatches 14; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073766; AAH73766.1; -; mRNA.

GO; GO:0016021; C:integral to membrane; IEA.

InterPro; IPR007110; Ig-like.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003599; Ig c1.

InterPro; IPR003596; Ig W.

R InterPro; IPR003006; Ig W.

R InterPro; IPR003506; Ig V.

R InterPro; IPR003506; Ig V.

R SMART; SM00409; IG; 2.

SMART; SM00406; IG; 2.

SMART; SM00406; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                       QGGMX6_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
Homo sapiens (Human).
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KITSSUE=591een;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farance A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Roman P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Rohards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Radan A., Rodrigues S., Sanchez A.,

Rahes J., Helton B., Ketteman M., Green E.D., Dickson M.C.,

Ralakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ralakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ralakesley R.W., Touchman J.W., Green E.D., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Reneration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences ";
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                                     79 NPSLKSRVTMSVDTSKNOFSLKLSSVTAADTAVYXCARGRFTYFDYMGOGTLVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGG-YLWNWIRQPPGKGLEWIGYISYDGTNN
61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS
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Submitted (UTM-2004) to the EMBL/GenBank/DDBJ databases.

BMBL; BC073773; AAH73773.1; -; mRNA.

GO; GO:0016021; C:integral to membrane; IEA.

InterPro; IPR007599; Ig.

InterPro; IPR003599; Ig.

InterPro; IPR003596; Ig.MHC.

InterPro; IPR003596; Ig. v.

Pfam; PP07654; Cl-set; 3.

SMART; SM00409; IGC; 2.

SMART; SM00406; IGC; 1.

SMART; SM00406; IGV; 1.
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SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                     476 AA.
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PROSITE; PS00290; IG MHC; UNKNOWN_2.
                                                                                                                                                                                                                                              QGGMX1_HUMAN PRELIMINARY;
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NUCLEOTIDE SEQUENCE.
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REPUINE-STABLEST, PubMed-12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

RIGCHINE, S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

Rapleton M., Soares M.B., Bonaldo M.F., Carainci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McKwan P.J., McKernan K.J., Maake J.A., Gunaratne P.H.,

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Richards S., Worley K.C., Sodergren B.J., Lu X., Glbbs R.A.,

Richards S., Worley K.C., Sodergren B.J., Lu X., Glbbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rochneration and initial analysis of more than 15,000 full-length human
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;
60 YKPSLKDRVIISVDTSKNQFSLKLSSVTAADTAVYYCARYG----RVF----FDYWGQG 110
                80 YNPSLKSRVTISLDTSKNOFSLKANSVTAADTAVYFCARAGVWGSPRSWAIDGFNIWGQG 139
                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51631 MW; 9FE59C09C50CFF85 CRC64;
                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO, GO:0016021; C:integral to membrane; IEA.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003596; Ig.WHC.
InterPro; IPR003596; Ig.W.
Pfam; PR07654; C1-set; Z.
SMART; SM00409; IG; 4.
SMART; SM004007; IGc1; 3.
                                                                                                                                                            477 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC073765; AAH73765.1; -; mRNA.
SMR; Q6GMX7; 247-455.
                                                                                                                                                      QGGMX7_HUMAN PRELIMINARY;
Q6GMX7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 78.33
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                   Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 477 AA; 5
                                                        TLVTVSS 117
                                                                                    140 TMVTVSS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                        111
                                                                                                                                              HUMAN
                                                                                                                                              Q6GMX7
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1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60

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Milder R.L., Notkins A.L., Casali P.;

Monplete sequence of the genes encoding the VH and VL regions of low-
encoding the VH and VL reg
                                                                                                                                                 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVF---FDYWGQGTLVTVSS 117
                                                                                                                                                                                                      79 NPSLKSRVTLSLDTSKNQFSLRLNSVTAADTAVYYCA-HGSSWDFAFDYWGQGTLVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCTVSGYSISG-GYLWNWIRQPPGKGLEWIGYISYDGTNN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 QLQLQESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPEKGLEWIGSLHNSGSDY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 YKPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 YNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARLGMGAFDFWGHGTMVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
20 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQTAGKGLEWIGYISHSGSTTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sub C.-H., Song C.-H., Lee C.-H., Lee S.-K.; in the synovium of "Clonal proliferation of IgM secreting B cell in the synovium of Behcet's patient with arthritis."; Submitted (OCT-1998) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VH4 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 AA; 16315 MW; 85664E04938AA7C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
WH4 heavy chain variable region precursor (Fragment)
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Last sequence update)
Last annotation update)
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QEP418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           095973 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91; Conservative
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>150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=1718404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGHD protein.
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Q6P418 H
1D Q6F
AC Q6F
DT 05-
DT 05-
DT 05-
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Name=LOC238447;
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                                                                                                      RECOURSE Primary B-Cells,

RECOURSE PRIMARY B-Cells,

RECOURSE PRIMARY B-Cells,

RECOURSE L.H., Derge J.G.,

RECOURSE L.H., Derge J.G.,

RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Permer A., Rubin G.M., Hong L.,

Rapleton M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Rapla S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robar S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Richards S.A., WcEwan P.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S.W., Voung A.C., Shevchenko Y., Boutfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Reneration and initial analysis of more than 15,000 full-length human and mouse conva sequences.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 NPSLKSRVTISVDKSKNOFSLKLSSVTAADTAVYYCASLGDIYYYGMDVWGQGTTVTVSS 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98
           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.3%; Score 464.5; DB 2; Length 576; 75.8%; Pred. No. 2.3e-38; rive 7; Mismatches 19; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Strausberg R.; Strausberg R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC065384; AAH63384.1; -; mRNA. HSSP; P01820; 1A7N. Ensembl; ENSG0000196122; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SMO0406; IGV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 576 AA; 63364 MW; FBE97C949D720F1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last seqn
01-MAR-2004 (TrEMBLrel. 26, Last ann
LOC238447 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003599; IG.
InterPro; IPR00310; IG-like.
InterPro; IPR00310; IG-like.
InterPro; IPR003597; IG cl.
InterPro; IPR003596; IG wh.C.
InterPro; IPR003596; IG w.P.
Fam; PP00454; Cl-eet; I.
Fam; PP00409; IG; I.
SMART; SM00409; IG; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q99M22_MOUSE PRELIMINARY;
Q99M22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 75.8 les 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Primary B-Cells;
                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                   NCBI_TaxID=9606;
Name=IGHD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Q99M22_MC
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Last sequence update) Last annotation update)

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RC TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months old;

RX TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months old;

RX TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months old;

RA STAIN=MX. FVBIN]

RA STAIN=MX. FAIROID E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buerow K.H., Schamen C.M., Schuler G.D.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

By Lischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

By Lapleton M.J., Goales M.B., Denlyuki S., Carninci P., Frange C.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malak J.A., Gunatarne P.H.,

RACHARGS S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RACHARGS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RILlalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RACHARGS S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G.G.,

RILLing M., Madan A., Young A. C., Shevchenko Y., Bouffard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Sahlska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Shalska U., Smailus D.E.,

R. Honse, Chila Hall S., Jones S.J.M., Marra M.A.;

R. Honse, Chila Hall S., Shermer B.D., Dickson M.C.,

R. Hall S., Schein J.E., Jones S.J.M., Marra M.A.;

R. Honse, Chila Hall S., Schein J.E., Jones R.J.M., Marra M.A.;

R. Honse, Chila Hall S., Schein J.E., Jones S.J.M., Marra M.A.;

R. Hall R. Hall S., Schein J.E., Jones R.J.M., Marra M.A.;

R. Hall R. Hall S., Schein J.E., Jones R.J.M., Marra M.A.;

R. Hall R. Hall S., Schein J.E., Jones R.J.M., Marra M.A.;

R. Hall R. Hall S., Shall R. Hall R.
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 PSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 PSLKNRISITRDTSKNQPPLKLNSVTTEDTATYYCASRGYSWFPNWGQGTLVTVSA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IISSUE=Mammary tumor, WAP-TGF alpha model. 7 months old; NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  479 AA; 51992 MW; 768E39A138918892 CRC64;
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Last sequence update)
Last annotation update)
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig-11ke.
InterPro; IPR003006; Ig-MC.
InterPro; IPR003596; Ig-WC.
Pfam; PF07654; Cl-8et; Z.
MART; SM00406; IG-V; 1.
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PROSITE; PS50835, IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN_2.
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HSSP; P01820; 1G7J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q96EYO HUMAN PRELIMINARY;
Q96EYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.
                                                                                                                              Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                  NCBI_TaxID=10090;
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1D Q96 AC Q96 DT Q1-

DT Q1-

DT Q1-

DT Q1-

DT Q1-

DE IGF
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                     146
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Rauener R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Astapleton M., Soars M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toohiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.B.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Scherzation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCA----RYGRVFFDYWGQGTLVTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 NPSLKSRVTMSVDTSKNQPSLKLSSVTAADTAVYYCASQPWELPTVGLFYWGQGTLVTVS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
             . Commonalia, Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Eusarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pubment System, Kitchingman G.R.;

"mRNA transcripts initiating within the human immunoglobulin mu heavy
chain enhancer region contain a non-translatable exon and are
extremely heterogeneous at the 5' end";
Nucleic Acids Res. 19:2427-2433 (1991).

BRML; BISS90; SISS90.

BIRS; RISS90; SISS90.

BIRS; QSEX0; 27-251.

BRRH; QSEX0; 27-251.

BRRH; QSEX0; 27-251.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                            TISSUE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.2%; Score 457.5; DB 2; Length 620; 78.5%; Pred. No. 1.3e-37; ive 3; Mismatches 18; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68125 MW; 990A1A4A6E8FF27B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00407; IGC1; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG MIC; UNKNOWN 3.
SEQUENCE 620 AA; 68125 MW; 990A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; Cl-set; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00409; IG; 2.
sapiens (Human)
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Best Local Similarity
                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH MGC Project;
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117 S 117

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60 YKPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR---YGRVFFDYWGQGTLVTVS 116
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 QVQLQESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQAPGRGLEWMGYIYYSGSTX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OVOLOESGPGLVKPSETLSLTCTVSGYSI-SGGYLWNWIRQPPGKGLEWIGYISYDGTNN
                                                                                                                                                                                                                                                                                                                                     TISSUE-Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Stobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX338066; CAD97996.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686C02218 (Fragment)
Name=DKFZp686C02218;
Homo sapiens (Human)
                                          01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686K04218 (Fragment).
Name=DKFZp686K04218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENSEMBL; G72379; 248-456.
Ensembl; ENSG0000130076; Homo sapiens.
InterPro; IPR007110; 1g-11ke.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam; PF07654; C1-set; 2.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88; Conservative
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27z379 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
NON TER
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                          NCBL_TaxID=9606;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 YSPSLKSRLTIFVDTSKNHFSLRLTSVTAADTAVYYCVRHVEGPYG--WFDPWGGGTLVT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGYSISG-GYLWNWIRQPPGKGLEWIGYISYDGTNN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 ÓLÓLÓESGPGLVKPSETLSLTCTVSGGSVSNRNYYWGWIRQPPGKGLEWIGSIYYNENTY 91
C TISSURE-Human rectum tumor;

A Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

B Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

A Pobo G., Han M., Wiemann S.;

L Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL; BX538077; CAD98001.1; -; mRNA.

R HSSP, PO1820; 1677.

R RHSSP, O72374; 262-470.

R Ensembl; ENSG0000130076; Homo sapiens.

R InterPro; IPR0031597; Ig-11.

R InterPro; IPR003597; Ig-11.

R InterPro; IPR003596; Ig-MC.

DR InterPro; IPR003596; Ig-W.

DR SMART; SM00406; IG-N.

R PROSITE; PS00290; IG-MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
full-length cDNA clone CSODL004YM19 of B cells (Ramos cell line) of
Homo sapiens (human) (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.7%; Score 448; DB 2; Length 49; 74.0%; Pred. No. 9.3e-37; ive 7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX248300; CAD62627.1; -; mRNA.
HSSP; PO1820; 1G7J.
SMR; Q86SXZ; 33.129.
Ensembl; ENSG00000130076; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=B cells;
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 HUMAN
Q86SX2_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein-
NON TER 1
SEQUENCE 492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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NCBI_TaxID=9606;
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0868XZ HUM
0868XX
AC 0868XX
AC 0868XX
DT 01-JU
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DT 01-JU
DT 01-JU
DT 01-MA
DE POULD
DE POULD
OC MAMMA
OC MAMMA
OC HOMO
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MEDINES SECTION SECTIO
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                              33 QVQLQESGPGLVKDSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
                                                                               1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016369; AAH16369.1; -; mRNA.
HSSP; PO1876; LDW0.
SMR; Q96KX8; Z66-474.
Ensembl; ENSG00000130076; Homo sapiens.
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SEQUENCE 496 AA; 53392 MW; D346929849040D69 CRC64;
                                                                                                                                                                                                                       92 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                          61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 98
88.8%; Pred. No. 5.3e-37;
tive 2; Mismatches 8
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PROSITE; PS00290; IG MHC; UNKNOWN 1.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP07654; C1-set; Z.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                              87; Conservative
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NUCLEOTIDE
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HV46_MOUSE
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                                                                                                                                                                                                             80 YNPSLKSRVTISVDTSKNOLSLKVRSVTAADTAVYFCARHGYSRSGRTGAIDYWGGGTLV 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 VQLQESGPGLVKPSQSLSLTCSVTDFSITSGYYWHWIRQFPGNKLEWMGYISYDGSNGYN 79
QVQLQESGPGLVKPSETLSLTCTVSGYSI - SGGYLWNWIRQPPGKGLEWIGYISYDGTNN 59
                                        20 QLQLQESGPGLVKSSETISLICTVSGGSISSSSYYWGWIRQPPGKGLEWIANTYYSGITY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 PSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-YGRVFPDYWGQGTLVTVSS 117
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                     YKPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYG-----RVFFDYWGQGTLV
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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Urakov D.N., Deev S.M., Polyanovsky O.L.;
The structure of the expressible VH gene from a hybridoma producing monoclonal antibodies against porcine transferrin.";
Mucleic Acids Res. 17:9481-9481 (1989).
EMBL; X16740; CAA34714.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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InterPro; IPR003599; IG.
InterPro; IPR003599; IG-like.
InterPro; IPR003596; Ig-v.
SWART; SW00409; IG; 1.
SWART; SW00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VH gene product (Fragment).
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Q6LBQ5;
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QSU413;
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Name=LOC544903;
                                                                                                                                                                                                                                                                                                                                          114 TVSS 117
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C50413 MOUSE
T 0 050413 M
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DT 01-FEB-20
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STRAIN=EVBN'N; TISSUE-Colon;

MEDLINE=238827; PubMed=1247992; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusham K., Parmer A.A., Rubin G.M., Henseh F.,

N. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T. E.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Wetteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g heavy chain V region MOPC 315 precursor.
Mus musculus (Mouse).

Mus musculus (Mouse).

Mammalia; Rutheria; Craniata; Vertebrata; Buteleostomi;
Muroidea; Mutheria; Euzronoteoglires; Glires; Rodentia; Sciurognathi;
MUCBI_TAXID=10090;
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NUCLEOTIDE SEQUENCE.
MEDLINE=89238351; PubMed=2497341; DOI=10.1016/0161-5890(89)90133-8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | NIH MGC Project; | Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases. | Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases. | R Ensembl; BCNSMUSGO000054328; | Mus musculus. | GO; GO: 0003823; | F: antigen binding; | IEA. | R InterPro; | IPR001359; | Ig. | InterPro; | IPR001359; | Ig. | InterPro; | IPR001359; | Ig. d.; | InterPro; | IPR001306; | Ig. MHC. | R InterPro; | IPR001306; | Ig. MHC. | R Pfam; | PF07654; | I. = 64; | I. | EMART; | SM00409; | IG. 3. | SMART; | SM00406; | IG. 3. | IL. | SMART; | SM00406; | IG. 3. | IL. | SMART; | SM00406; | IG. MHC; | UNKNOWN 2. | SEQUENCE | 483 AA; | 52714 WW; | 7C272DA501A4A0D1 | CRC64; | SEQUENCE | 483 AA; | 52714 WW; | 7C272DA501A4A0D1 | CRC64; | SM00406; | IG. MHC; | INKNOWN 2. | SEQUENCE | 483 AA; | 52714 WW; | 7C272DA501A4A0D1 | CRC64; | SM00406; | IG. MHC; | INKNOWN 2. | SM00406; | IG. MHC; | INKNOWN 2. | SEQUENCE | 483 AA; | 52714 WW; | 7C272DA501A4A0D1 | CRC64; | IC. | INKNOWN 2. | IC. | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.0%; Score 443.5; DB 2; Length 70.6%; Pred. No. 2.6e-36; ative 13; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 AA
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STRAIN=FVB/N; TISSUE=Colon;
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                                                                                                                                                                                                                                                                                           MEDLINE=74170779; PubMed=4524622; Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.; Manino-acid sequence of the variable region of the heavy (alpha) chain of a mouse myeloma protein with anti-hapten activity."; Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
Rinfret A., Horne C., Dorrington K.J., Klein M.;
"Cloning, sequencing and expression of the rearranged MOPC 315 VH gene
segment.";
                                                                                                                                                                                             MEDLINE=79148758; PubMed=428562; Schechter I., Wolf O., Zemell R., Burstein Y.; "Structure and function of immunoglobulin genes and precursors."; Fed. Proc. 38:1839-1845(1979).
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE REVISION TO 53.
MEDLINE=77244979; PubMed=268248;
Medo L., Margolies M.N., Givol D., Zakut R.;
Unpublished results, cited by:
Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
-!- MISCELLANBOUS: This alpha chain was isolated from a myeloma protein that has anti-dinitrophenyl activity.
                                                                             PROTEIN SEQUENCE OF 1-31.
MEDLINE=78094475; PubMed=414225;
Jilka R.L., Peetka S. D., Peetka R.L., Peetka C., "Amino acid sequence of the precursor region of MOPC-315 mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain V region MOPC 315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity.

G -> GG (in Ref. 1; CAA30727).

G -> H (in Ref. 2).

GY -> YG (in Ref. 4).

N -> D (in Ref. 4).

Missing (in Ref. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.7%; Score 442; DB 1; Length 137; 69.5%; Pred. No. 9.3e-37; ive 15; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15399 MW; FB3828304C2B81DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00406; IGV; 1.—
PROSITE; PSS0835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Signal.
                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M27638; AAA61337.1; -; Genomic DNA.
BMBL; X07880; CAA30727.1; -; Genomic_DNA.
PIR; PL0102; AVMS35.
HSSP; P01820; 1G7J.
SMR; P01822; 20-137.
Engembl; EMSWISGGOOGOS7048; Mus musculus.
InterPro; IPR00710; IG-like.
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Framework-1
                                                 Mol. Immunol. 26:431-434(1989).
                                                                                                                                           immunoglobulin heavy chain."
                                                                                                                                                                                                                                                                                PROTEIN SEQUENCE OF 19-136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 69.55
Matches 82; Conservative
                                                                                                                                                                                     PROTEIN SEQUENCE OF 1-21.
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48
54
68
116
116
117
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123
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137 AA;
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Gaps

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20 VQLQESGPGLVKPSQSLSLTCSVTGYSITSGYFWNWIRQFPGNKLEWLGFIKYDGSNGYN 79
2 VQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK 61
                                                                                                                                                              62 PSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCA--RYGRVFFDYWGQGTLVTVSS
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completed: January 10, 2006, 20:53:28 Search comp Job time :

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January 10, 2006, 20:55:23; Search time 5.96642 Seconds (without alignments) 166.558 Million cell updates/sec
                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117
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1: /cgn2_6/ptodata/1/pubpaa/USO8 NEW FUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO8 NEW FUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO7 NEW FUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/PCT NEW FUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO9 NEW FUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US10 NEW FUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US10 NEW FUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US10 NEW FUB.pep:*
GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### 72, Appl 1, Appli 1619, Ap 1651, Ap 1548, Ap Sequence 79, Description Sequence US-11-012-353-75 US-11-012-353-75 US-11-012-353-83 US-11-012-353-69 US-11-012-353-69 US-11-012-353-69 US-11-012-353-70 US-11-012-353-73 US-11-054-515-1651 US-11-054-515-1651 US-11-054-515-1651 US-11-054-515-1651 US-11-054-515-1651 US-11-054-515-1619 US-11-054-515-1994 US-11-054-515-1329 US-10-512-184-34 US-10-512-184-71 US-10-512-184-49 US-10-721-763-17 SUMMARIES Query Match Length DB 1000.0 999.0 999.0 999.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 627 623 623 615 615 615 541 541 541 481.5 481.5 481.5 473 473 469.5 469.5 469.5 469.5 467.5 461.5 461.5 461.5 Result

Sequence 1578, Ap	Sequence 990, App	Sequence 1981, Ap	Sequence 1339, Ap	Sequence 25, Appl	Seguence 1659, Ap	Sequence 21, Appl	Sequence 1607, Ap	Sequence 12, Appl	Sequence 1745, Ap	Sequence 844, App	Sequence 1597, Ap	Sequence 1546, Ap	Sequence 55, Appl	Sequence 20, Appl	Sequence 20, Appl	_:	Sequence 954, App	Sequence 1321, Ap	Sequence 1223, Ap
US-11-054-515-1578	US-11-054-515-990	US-11-054-515-1981	US-11-054-515-1339	US-10-721-763-25	US-11-054-515-1659	US-10-721-763-21	US-11-054-515-1607	US-11-139-499-12	US-11-054-515-1745	US-11-054-515-844	US-11-054-515-1597	US-11-054-515-1546	US-11-084-554-55	US-11-144-248-20	US-11-144-222-20	US-11-054-515-1510	US-11-054-515-954	US-11-054-515-1321	US-11-054-515-1223
7	7	7	7	9	7	9	7	7	7	7	7	7	7	7	7	7	7	7	7
254	251	247	253	154	254	146	256	476	256	254	255	251	66	113	113	251	253	249	252
73.4	73.4	73.3	73.2	72.8	72.6	72.3	71.9	71.6	71.5	71.5	71.5	71.4	71.1	71.0	71.0	71.0	71.0	70.7	7.07
460.5	460	459.5	459	456.5	455.5	453.5	450.5	449	448.5	448	448	447.5	445.5	445	445	445	445	443.5	443
26	27	28	29	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

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US-11-012-353-79

Sequence 79, Application US/11012353

Publication No. US20050249730A1

Sequence 79, Application US/11012353

Publication No. US20050249730A1

APPLICANT: GOETSCH, LILIANE

APPLICANT: CGRYALA, NATHALIE

APPLICANT: DUFLOS, ALAIN

APPLICANT: LEGER, OLIVIER

APPLICANT: LEGER, OLIVIER

APPLICANT: LEGER, OLIVIER

APPLICANT: LEGER, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF

FILE REPERENCE: 01753-196

PRIOR REPERENCE: 01753-196

PRIOR APPLICATION NUMBER: US/11/012,353

CURRENT PILING DATE: 2003-12-16

PRIOR PILING DATE: 2003-0-11

PRIOR PLILING DATE: 2003-0-20

PRIOR PLILING DATE: 2002-01-20

PRIOR PLILING DATE: 2002-01-18

PRIOR PLILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR PLILING DATE: 2002-01-18

PRIOR PLING DATE: 2002-01-18
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Pred. No. 1.2e-48;
); Mismatches 0; Indels
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100.0%; Prev
0; N
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Matches 117; Conservative
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; ORGANISM: Homo sapiens
US-11-012-353-79
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Best Local Similarity
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Gaps

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Sequence 77, Application US/11012353

Sequence 77, Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:
APPLICANT: GOGTSCH, LILIANE
APPLICANT: CORYALA, NATHALIE
APPLICANT: LEGER, OLLVIER
APPLICANT: HABUM, USAN-FRANCOIS
APPLICANT: HABUM, UNVER. NOVEL ANTI-IGP-IR AND/OR ANTI-INSULIN/IGP-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PR 0200553
PRIOR FILING DATE: 2002-07-10
PRIOR PILING DATE: 2002-07-10
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.4%; Score 623; DB 7; Length 117; Best Local Similarity 98.3%; Pred. No. 2.7e-48; Matches 115; Conservative 2; Mismatches 0; Indels
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PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTIN VET: 3.3
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CORGANISM: Homo sapiens
US-11-012-353-77
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US-11-012-353-75
                                                                                                                                                                                                                                                                                        LENGTH: 117
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                                                                                        US-11-012-353-81

Sequence 81, Application US/11012353

PUBLICANT 0. US20050249730A1

GENERAL INFORMATION:
APPLICANT GORDSTALL USEAUCH OF THE APPLICANT:
APPLICANT: CORVAIA, NATHALIE
APPLICANT: LEGER, OLIVIER
APPLICANT: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT PILLING DATE: 2003-07-11
PRIOR PILLING DATE: 2003-07-11
PRIOR PILLING DATE: 2003-07-120
PRIOR PILLING DATE: 2002-01-20
PRIOR PILLING DATE: 2002-01-18
PRIOR PILLING DATE: 2002-01-18
PRIOR PILLING DATE: 2002-01-18
PRIOR PILLING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARR: PECENTION VOYER: 73.3
SOFTWARR: PECENTION VOYER: 3.3
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Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: BUFLOS, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVERER: US/11/012,353

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-21

PRIOR PLILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR PLILING DATE: 2003-01-20

PRIOR PLILING DATE: 2003-01-20

PRIOR PLILING DATE: 2003-01-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-81
                                                                                     11-012-353-81
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Matches 115; Conservative
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; ORGANISM: Mus musculus
US-11-012-353-69
                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-11-012-353-85
                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Best Local
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TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REPRESENCE: 017753-198
CURRENT APPLICATION NUMBER: U5/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR FILING DATE: 2003-01-21
PRIOR FILING DATE: 2003-01-11
PRIOR PELICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2003-01-20
PRIOR PLILING DATE: 2002-01-18
PRIOR PELING DATE: 2002-01-18
PRIOR PELING DATE: 2002-01-18
PRIOR PELING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-01-18
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APPLICANT: CORVAIA, MATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEGN, JEAN-FRANCOIS
APPLICANT: HAEGN, USAN-FRANCOIS
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR APPLICATION NUMBER: PR 0308538
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
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98.1%; Score 615; DB 7;
Best Local Similarity 98.3%; Pred. No. 1.4e-47;
Matches 115; Conservative 1; Mismatches 1;
Sequence 83, Application US/11012353;
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, ALAIN
APPLICANT: LEGER, ALAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-83
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GENERAL INFORMATION:
APPLICANT: GOEVARATION:
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2003-12-16
PRIOR PLLING DATE: 2003-07-11
PRIOR PLLING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 020558
PRIOR APPLICATION NUMBER: FR 020559
PRIOR APPLICATION NUMBER: FR 020553
PRIOR PLLING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: FR 020553
PRIOR PLLING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: FR 020553
PRIOR PLLING DATE: 2002-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYL#NWIRQFPGNKLEWMGYISYDGTNNYK 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 615; DB 7;
Pred. No. 1.6e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver: 3.3
SEQ ID NO 85
LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 69, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
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98.3%;
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US-11-012-353-162
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APPLICANT: COCHALA, NATHALIE
APPLICANT: COCHALA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
APPLICANT: BLEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULING DATE: 2003-12-16
PRIOR PELLING DATE: 2003-12-16
PRIOR PELLING DATE: 2003-07-11
PRIOR PPLICATION NUMBER: PR 020553
PRIOR PELLING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 020553
PRIOR PLING DATE: 2002-01-18
PRIOR PELLING DATE: 2002-01-18
PRIOR PELLING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTIN VUMBER: FR 020553
SEQ ID NO 52
LENGTH: 127
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Fublication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GOETSCH, LILIANE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DUFLOS, ALAIN

APPLICANT: BECK, ALAIN

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-198

CURRENT FILING DATE: 2004-12-16

FRIOR FILING DATE: 2004-12-16

PRIOR APPLICATION NUMBER: 10/735, 916

PRIOR PLILOTION NUMBER: RR 0308538

PRIOR PLILOTICIN NUMBER: PCT/FR03/00178
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PSLKDRISITRDTSKNOFFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
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                                                                                                                                  Sequence 52, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-52
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GENERAL INFORMATION:

APPLICANT: GOETSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPPORS ANTIBODIES AND USES THEREOF
FILE REFERRINCE: 01753-198
FILE REFERRINCE: 01753-196
PRIOR PLILING DATE: 2003-01-16
PRIOR PLILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 020553
PRIOR PLILING DATE: 2003-01-20
PRIOR PLILING DATE: 2002-01-20
PRIOR APPLICATION NUMBER: FR 020653
PRIOR PLILING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-01-18
PRIOR PRILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 020654
PRIOR PRILING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGGGTTLTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGYSISSGYYWGWIRQPPGKGLEWIGSIFHSGSSYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                        PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR PELING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 162
LENGTH: 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.5%;
86.3%;
FILING DATE: 2003-01-20
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Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mus musculus
US-11-012-353-70
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61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARY-----GRVF-FDYWGQGTLV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLMNWIRQPPGKGLEWIGYISYDGTNNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR PLILING UNERER: 60/340,817
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-06-15
PRIOR PLILNG DATE: 2001-06-15
PRIOR PLILNG DATE: 2001-05-25
PRIOR PLILNG DATE: 2001-03-21
PRIOR PLILNG DATE: 2001-03-21
PRIOR PLILNG DATE: 2001-03-16
PRIOR PLILNG DATE: 2003-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSNYSISSGYYWGWIRQPPGKGLEWIGSIYYSGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.8%; Score 481.5; DB 7; Length 247; Best Local Similarity 77.4%; Pred. No. 1.2e-35; Matches 96; Conservative 5; Mismatches 16; Indels 7.
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US-11-054-515-1548
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                                                                                                                                Sequence 73, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HEGER, OLIVIER
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVER ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVERER: 2004-12-16
FRICK RAPPLICATION NUMBER: 10/735,916
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SSOFTWARE: PALENTIN VET. 3:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRV-----FFDYWGQGTLV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGYSISSGYYWSWIRQPPGKGLEWIGSMFHSGSSYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
       62 PSLKNRISITRDISKNQFFLKIANSVTTEDIATYYCAREGYGYFPDYWGGGTTLIVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Gaps
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; Sequence 1651, Application US/11054515
; Publication No. US200025532A1
; RUBLICATION NO. US2000025532A1
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REPERBNCE: PF523P3
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR FILING DATE: 2004-06-18
; PRIOR FILING DATE: 2004-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 482; DB 7; Length 123;
Pred. No. 5.5e-36;
8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.9%;
Best Local Similarity 77.4%;
Matches 96; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 123
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Gaps

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Search completed: January 10, 2006, 21:36:24 Job time : 5.96642 secs
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                                                                                                                                                                                                                                                                                                                                           61 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVHYDILTGYLWAFDIWGQGTMV 120
                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGLEWIGSIYHSGSTYY 60
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                                                                                                                                                                                               1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
APPLICANT: GOETSCH, LILIANE
APPLICANT: DEPLOS, ALAIN
APPLICANT: HAGUW, JEAN-FRANCOIS
APPLICANT: HAGUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                            7;
                                                                                Length 250;
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                                                                                Query Match 76.8%; Score 481.5; DB 7; Best Local Similarity 77.4%; Pred. No. 1.2e-35; Matches 96; Conservative 6; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
75.4%; Score 473; DB 7;
Best Local Similarity 79.5%; Pred. No. 3.2e-35;
Matches 93; Conservative 6; Mismatches 18.
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CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
FRIOR APPLICATION NUMBER: 10/735,916
PRIOR PILING DATE: 2003-12-16
PRIOR PILING DATE: 2003-12-16
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-17
PRIOR PILING DATE: 2003-07-17
PRIOR PILING DATE: 2003-07-17
PRIOR PILING DATE: 2003-07-07
PRIOR PILING DATE: 2003-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2003-01-18
PRIOR PILING DATE: 2003-01-18
PRIOR PILING DATE: 2003-01-18
PRIOR PILING DATE: 2003-01-18
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COCATION: (59)
COTHER INFORMATION: Variable amino acid
US-11-012-353-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 72, Application US/11012353
Publication No. US20050249730A1
; ORGANISM: Homo sapiens
US-11-054-515-1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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61 KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYG-----RVFFDYWGQGTLVTV 115
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Sequence 1, Application US/11102201
| Publication No. US2005026594A1
| GABREAL INFORMATION:
| APPLICANT: MANTYH, Patrick W. |
| TITLE OF INVENTION: METHODS FOR TREATING BONE CANCER PAIN BY TITLE OF INVENTION: METHODS FOR TREATING BONE CANCER PAIN BY TITLE OF INVENTION: ADMINISTERING A NERVE GROWTH FACTOR ANTAGONIST FILE REFERENCE: 51471-20021.00 | CURRENT FILING DATE: 2004-004-07 | PRIOR APPLICATION NUMBER: US 60/620,654 | PRIOR APPLICATION NUMBER: US 60/620,654 | PRIOR APPLICATION NUMBER: US 60/560,781 | PRIOR APPLICATION NUMBER: US 60/560,781 | PRIOR PILING DATE: 2004-04-07 | NUMBER OF SEQ ID NOS: 8 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO 1 | LENGTH: 120 | LENGTH: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGFSLI-GYDLAWIRQPPGKGLEWIGIIWGDGTTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Synthetic Construct US-11-102-201-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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January 10, 2006, 20:53:43; Search time 64.1754 Seconds (without alignments) 761.757 Million cell updates/sec
                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSETLSL.....RYGRVFFDYWGQGTLVTVSS 117
GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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627
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Total number of hits satisfying chosen parameters:

1867569 segs, 417829326 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Published Applications AA Main:*
1. /cgn2 6/ptodata/1/pubpa4/uso7 PUBCOMB.pep:*
2. /cgn2 6/ptodata/1/pubpa4/uso8 PUBCOMB.pep:*
3. /cgn2 6/ptodata/1/pubpa4/uso9_PUBCOMB.pep:*
4. /cgn2 6/ptodata/1/pubpa4/usoABPCOMB.pep:*
5. /cgn2 6/ptodata/1/pubpa4/usoBPUBCOMB.pep:*
5. /cgn2 6/ptodata/1/pubpa4/usoBPUBCOMB.pep:*
5. /cgn2 6/ptodata/1/pubpa4/usoBPUBCOMB.pep:* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

:	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	, App			Appl	Appl	Appl	Appl	_	, App	Appl	Appl	Appl	Appli	Appli	Appl	Appl	Appl	Appli
g	79,	75,	11,	83,	85,	69	25,	26,	143	24,	109	28,	26,	25,	29,	128	127	11,	24,	27,	ທີ	'n	82,	86,	23,	7
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ID	US-10-735-916A-79	US-10-/35-916A-81 US-10-735-916A-75	US-10-735-916A-77	US-10-735-916A-83	US-10-735-916A-85	US-10-735-916A-69	US-10-735-916A-52	US-10-383-447-26	US-10-309-762-143	US-10-383-447-24	US-10-292-088-109	US-10-383-447-28	US-10-805-177-56	US-10-309-762-25	US-10-309-762-29	US-10-309-762-128	US-10-309-762-127	US-10-010-729-11	US-10-309-762-24	US-10-309-762-27	US-10-125-687-5	US-10-996-191-5	US-10-292-088-82	US-10-292-088-86	US-10-937-596-23	US-10-890-945-2
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Length DB	117	117	135	117	135	117	127	120	119	120	118	120	121	122	122	120	116	121	122	122	119	119	121	466	119	117
* Query Match	100.0	99.4	99.4	98.1	98.1	86.3	86.3	84.0	80.9	80.8	80.5	80.3	80.3	80.3	80.3	80.1	79.8	79.8	79.8	79.8	79.7	79.7	79.7	79.7	79.4	79.3
Score	627	623	623	615	615	541	541	526.5	507	506.5	504.5	503.5	503.5	503.5	503.5	502.5	500.5	500.5	500.5	500.5	200	200	200	200	498	497
Result No.	<b>н</b> с	N 60	4	ហ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

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Sequence 98, Appl Sequence 70, Appl Sequence 37, Appl Sequence 39, Appl Sequence 20, Appl Sequence 114, Appl Sequence 14, Appl Sequence 14, Appl Sequence 10, Appl Sequence 11, Appl
US-10-292-088-98 US-10-292-088-70 US-10-310-719-35 US-10-310-719-35 US-10-984-960A-20 US-10-984-960A-20 US-10-981-976-39 US-10-893-976-39 US-10-805-177-114 US-10-805-177-114 US-10-802-306A-5 US-10-802-306A-5 US-10-309-762-138 US-10-309-762-138 US-10-988-360-10 US-10-988-360-10 US-10-988-360-10 US-10-982-306A-9 US-10-822-306A-9 US-10-822-306A-9 US-10-822-306A-9
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9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

## ALIGNMENTS

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1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
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Sequence 79, Application US/10735916A

Sequence 79, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:

APPLICANT: GORYALA, Liliane

APPLICANT: CORVALA, Nathalie

APPLICANT: LEGER, Olivier

APPLICANT: LEGER, Olivier

APPLICANT: HAEUW, Jean-Francois

TITLE REFERENCE: Ol7753-183

TITLE REFERENCE: 017753-183

CURRENT APPLICATION NUMBER: US/10/735,916A

CURRENT FILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-01-1

PRIOR PELICATION NUMBER: FR 03/00 653

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-05-07

NUMBER: FR 02/05 753
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100.0%; Pred. No. 8.7e-48;
tive 0; Mismatches 0;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 117; Conservative
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US-10-735-916A-79
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RESULT 2 US-10-735-916A-81 'Sequence 81, Application US/10735916A 'Publication No. US20050084906A1

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US-10-735-916A-75
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             JUNEARAL INFURANTION

JUNEARAL INFURANTION

APPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: DUFLOS, Alain

APPLICANT: BECK, Alain

APPLICANT: BECK, Alain

APPLICANT: HAEUW, Jean-Francois

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-183

CURRENT APPLICATION NUMBER: US/10/735,916A

CURRENT PILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-07-11

PRIOR PELING DATE: 2003-01-10

PRIOR PILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: FR 02/00 654

PRIOR PILING DATE: 2002-01-18

PRIOR PELING DATE: 2002-05-07

NUMBER OF SEQ ID NOS: 156

SOFTWARE: PALEALIN Ver. 2.1

LEMER OF SEQ ID NO 81
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### CENTERAL INFORMATION
### APPLICANT: GORYALA, Nathalie
### APPLICANT: GORYALA, Nathalie
### APPLICANT: CRVALA, Nathalie
### APPLICANT: LEGER, Olivier
### APPLICANT: BECK, Alain
### APPLICANT: BECK, Alain
### APPLICANT: BECK, Alain
### APPLICANT: HAEUW, Jean-Francois
### TILE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
### TILE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
### TILE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
### TILE OF INVENTION: NOVER: 103/08 538
### PRIOR FILING DATE: 2003-07-11
### PRIOR FILING DATE: 2003-07-11
### PRIOR FILING DATE: 2002-01-18
### PRI
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100.0%; Score 627; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 117; Conservative 0; Mismatches 0; Indels
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
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Sequence 77, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION

APPLICANT: GOSTSCH, Liliane

APPLICANT: GOSTSCH, Liliane

APPLICANT: GOSTSCH, Liliane

APPLICANT: GOSTSCH, Alain

APPLICANT: BEEK, Alain

APPLICANT: HAEW, Jean-Francois

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-183

CURRENT APPLICATION NUMBER: RR 03/08 538

PRIOR PILING DATE: 2003-01-26

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR PLING DATE: 2002-01-18
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15-916A-83

16-83. Application US/10735916A

17-10-735-916A-83

18-80ance 83. Application US/10735916A

18-80ance 83. Application No. US20050084906A1

18-80ance 84. Application No. US20050084906A1

18-80ance 84. Applicant CORVAIA. Nathalie

18-80ance 85. Alain

18-80ance 86. Alain

18-80ance 86
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Pred. No. 2.3e-47;
2; Mismatches 0; Indels
Query Match 99.4%; Score 623; DB 5; Length 117; Best Local Similarity 98.3%; Pred. No. 2e-47; Matches 115; Conservative 2; Mismatches 0; Indels
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Best Local Similarity 98.34
Matches 115; Conservative
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; ORGANISM: Homo sapiens
US-10-735-916A-77
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19 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 78
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15.40-735-916A-85

15.40-735-916A-85

16.210-735-916A-85

17.50-735-916A-85

18.50-735-916A-85

18.50-735-916A-85

18.50-735-916A-85

18.50-735-916A-96A-1

18.50-735-916A-1

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                                CURRENT PEPLICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: RR 03/08 538
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
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PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PARCHIN VET. 2.1
SEQ ID NO 83
LENGTH: 117
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Best Local Similarity 98.3%;
Matches 115; Conservative 1
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ORGANISM: Homo sapiens
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61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
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                                                                                                                                                                                                                                                                                                               JUDICANT: GOETSCH, Liliane

APPLICANT: GOETSCH, Liliane

APPLICANT: GOETSCH, Liliane

APPLICANT: GOETSCH, Liliane

APPLICANT: BEER, Olivier

APPLICANT: BEEK, Alain

APPLICANT: HAEUW, JOAN-Francois

TITLE OF INVENTION: NOWEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-183

CURRENT APPLICATION NUMBER: US/10/735,916A

CURRENT FILING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: FR 03/08 538

PRIOR PILING DATE: 2003-01-18

PRIOR APPLICATION NUMBER: FR 02/00 653

PRIOR APPLICATION NUMBER: FR 02/00 654

PRIOR APPLICATION NUMBER: FR 02/00 654

PRIOR PILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-05-07

NUMBER OF SEQ ID NOS: 156

SOFTWARE PATENTIN VEY: 2.1
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| Publication No. US2050084906A1 |
| GBUERAL INFORMATION: US2050084906A1 |
| GBUERAL INFORMATION: Liliane |
| APPLICANT: CORVAIA, Nathalie |
| APPLICANT: CORVAIA, Nathalie |
| APPLICANT: UBGER, Olivier |
| APPLICANT: BECK, Alain |
| APPLICANT: BECK, Alain |
| APPLICANT: BECK, Alain |
| APPLICANT: HARUW, Jean-Francois |
| TILE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF |
| TILE REFERENCE: 017753-183 |
| TILE REFERENCE: 017753-183 |
| FILE REFERENCE: 2003-07-11 |
| PRIOR APPLICATION NUMBER: FR 03/08 538 |
| PRIOR FILING DATE: 2003-07-11 |
| PRIOR FILING DATE: 2003-07-11 |
| PRIOR FILING DATE: 2003-01-20 |
| PRIOR FILING DATE: 2003-01-20 |
| PRIOR FILING DATE: 2003-01-20 |
| PRIOR FILING DATE: 12003-01-20 |
| PRIOR FILING DATE: 12003-01-20 |
| PRIOR FILING DATE: 12003-01-20 |
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Publication No. US20040018198A1
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JAPPLICANT: Bhaskar, Vinay

APPLICANT: Bhaskar, Vinay

APPLICANT: Law, Debbie

APPLICANT: Caras, Ingrid

APPLICANT: Law, Debbie

APPLICANT: Murray, Richard

APPLICANT: Powers, David

TITLE OF INVENTION: Antibodies Against Cancer Antigen TMEFF2 and Uses Thereof

FILE REFREENCE: 05882.013 NUMBER: US 60/362,837

FRIOR APPLICATION NUMBER: US 60/362,837

FRIOR PLING DATE: 2002-03-07

FRIOR PLING DATE: 2002-12-27

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 26

LENGTH: 120

MUNDER OF SEG ID NOS: 34

SEG ID NO 26

LENGTH: 120
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Best Local Similarity 84.0%; Pred. No. 6.7e-39;
Matches 100; Conservative 6; Mismatches 10; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                            Length 127;
                                                                                                                                                                                                                                                                                                          Query Match 86.3%; Score 541; DB 5; Length 12° Best Local Similarity 84.5%; Pred. No. 3.7e-40; Matches 98; Conservative 10; Mismatches 8; Indels
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; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR PLILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 52
; LENGTH: 127
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                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-52
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ORGANISM: Artificial
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RESULT 10 US-10-309-762-143 ; Sequence 143, Application US/10309762

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61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRV---PFDYWGQGTLVTVSS 117
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GENERAL INFORMATION:

APPLICANT: Gudas, Jean
APPLICANT: Gudas, Jean
APPLICANT: Handa, Masahisa
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR APPLICATION NUMBER: 60/337275
SOFTWARE: FASTER OF SEQ ID NOS: 246
SOFTWARE: FASTER OF SEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.8%; Score 506.5; DB 4; Length 120; 79.8%; Pred. No. 3.9e-37; ive 10; Mismatches 11; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 80.9%; Score 507; DB 4; Length 119; Best Local Similarity 83.3%; Pred. No. 3.5e-37; Matches 100; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Variable heavy chain region 2.0
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                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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Matches 95; Conserv
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US-10-309-762-25
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LENGTH: 121
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APPLICANT: daw, Debbie
APPLICANT: daw, Debbie
APPLICANT: Caras, Ingrid
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Powers, David
TITLE OF INVENTION: Antibodies Against Cancer Antigen TMEFF2 and Uses Thereof
FILE REPERENCE: 05882.0138.NPUSOO
CURRENT APPLICATION NUMBER: US 10/10/383,447
CURRENT APPLICATION NUMBER: US 60/362,837
PRIOR APPLICATION NUMBER: US 60/463,812
PRIOR FILING DATE: 2002-03-08
PRIOR FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
SEQ ID NO 28
LENGTH: 120
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62 PSLKDRVTISRDTSKNOPSLKLSSVTAADTAVYYCA---RYGRVFFDYWGQGTLVTVSS 117
                        61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCAR--YGRVFFDYWGQGTLVTVSS 117
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; OTHER INFORMATION: Variable heavy chain region 4.0
US-10-383-447-28
                                                                                                                                                Sequence 109, Application US/10292088

Publication No. US20030211100A1

GENERAL INPOMATION:

APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: GORVALAN, JOSE

APPLICANT: JIA, XIAO-CHI

APPLICANT: JIA, XIAO-CHI

APPLICANT: FENG, XIAO

TITLE OF INVENTION: ANTIBODIES TO CD40

FILE REFERENCE: ABX-PP/3 US

CURRENT APPLICATION NUMBER: US/10/292,088

CURRENT APPLICATION NUMBER: 60/348,980

PRIOR FILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PATENT VET. 2011

SEQ ID NO 109

LENGTH: 118
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Publication No. US20040096392A1
GENERAL INFORMATION:
APPLICANT: Bhaskar, Vinay
APPLICANT: de la Calle, Agustin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 84.0°
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-10-292-088-109
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                                                                                                            RESULT 12
US-10-292-088-109
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APPLICANT: Landes, Gregory M.
APPLICANT: Landes, Gregory M.
APPLICANT: Landes, Binyam
APPLICANT: Chen, Francine
APPLICANT: Beazbeh, Binyam
APPLICANT: Foltz, Ian
APPLICANT: Tse, Kam Fai
APPLICANT: Tse, Kam Fai
APPLICANT: Starling, Gary
APPLICANT: Meari, Medi
APPLICANT: Messe, Peter
APPLICANT: Michael
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 YKPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYG--RVFFDYWGQGTLVTVSS 117
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APPLICANT: FOLZ, Ian
APPLICANT: FOLZ, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: 05/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
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         Length 120;
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                                                                                                       13; Indels
    DB 4;
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Query Match 80.3%; Score 503.5; DB 4 Best Local Similarity 81.5%; Pred. No. 7.2e-37; Matches 97; Conservative 6; Mismatches 13
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Publication No. US20050084449A1
GENERAL INFORMATION:
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US-10-805-177-56
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2;
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; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 25; LENGTH: 122; TYPE: PRT: 7 TYPE: PRT: 0KGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                Search completed: January 10, 2006, 21:35:33
Job time : 65.1754 secs
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Scoring table:

Searched:

Sequence:

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Sequence 11,
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APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Limin
APPLICANT: Ge, Limin
APPLICANT: Moroney, Simon
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James P. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
CUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

79.7%; Score 500; DB 2; Length 119;
Best Local Similarity 83.3%; Pred. No. 4.6e-42;
Matches 100; Conservative 4; Mismatches 12; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
PILING DATE: 18-FBB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
ATTONEY, AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
US-09-343-698-6
US-08-325-955-6
US-09-273-453-7
US-09-273-453-7
US-08-36-0125-5
US-08-450-578-5
US-09-017-628-5
US-09-017-628-5
US-09-467-903-5
US-09-467-903-5
US-09-467-903-5
US-09-467-903-5
US-09-471-276-837
US-09-260-527-3
US-08-480-774A-2
US-08-275-053-13
US-08-450-578-11
US-08-450-578-11
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                                                                                                                                                                                                                                                                                                                                                              Sequence 39, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 119 amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-09-025-769B-39
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465.5
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465.5
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                                                                                                   January 10, 2006, 20:34:27; Search time 22.847 Seconds (without alignments) 423.384 Million cell updates/sec
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Sequence 25,
Sequence 25,
Sequence 77,
Sequence 11,
Sequence 11,
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Sequence 65,
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Sequence 65,
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Sequence
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6_COMB.pep:*

(cgn2_6/ptodata/1/iaa/H_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                   GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd
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US-09-490-1070-65
US-09-490-153-39
US-09-490-153-39
US-09-490-153-65
US-09-490-153-65
US-09-490-134-39
US-09-490-324-39
US-09-490-324-39
US-09-490-324-65
US-09-130-613A-13
US-08-456-717-64
US-08-456-717-64
US-08-456-717-64
US-08-456-717-64
US-08-456-717-64
US-08-490-070A-25
US-09-490-138-99
US-09-490-138-99
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US-09-800-729-145
US-10-330-613A-5
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Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
                               Copyright
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Perfect score:
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                                                                                                                  60 NPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119
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                                                                                          61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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9
                          1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY 59
QVQLQESGPGLVKPSETLSLTCTVSGYS1TGGYLWNW1RQPPGKGLEWIGY1SYDGTNNY
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ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30 (EPO)
SOFTWARE PATENTIN BATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REJEPHONE: (212)596-900
TELEPHONE: (212)596-900
TELEPHONE: (212)596-900
TELEPHONE: (212)596-900
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.7%; Score 500; DB 2; Length 119; Best Local Similarity 83.3%; Pred. No. 4.6e-42; Matches 100; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                        GENERAL INPORMATION:
APPLICANT: ROADPIK, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: 169, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plockthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                Sequence 65, Application US/09025769B Patent No. 6300064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-09-025-769B-65
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US-09-490-070A-39; Sequence 39, Application US/09490070A; Patent No. 6696248

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60 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                   ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 119;
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Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                   Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.7%; Score 500; DB 2;
83.3%; Pred. No. 4.6e-42;
iive 4; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,298
REFERRENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDMESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 65, Application US/09490070A Patent No. 6696248 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202) 912-2020
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 83.3
Matches 100; Conservative
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ZIP: 10021
COMPUTER READABLE FORM:
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-490-153-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Gaps
                                                                                                                                                                                                                                              MEDIUM TYPE Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CONFINENT PAPLICATION

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REFERENCE/DOCKET NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 31,298

TELECOMUNICATION NUMBER: 31,298

TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION INFORMATION INFORMATION INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.7%; Score 500; DB 2; Length 119; 83.3%; Pred. No. 4.6e-42; ive 4; Mismatches 12; Indels
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Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
                                    1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-070A-65
White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-490-153-39; Sequence 39, Application US/09490153; Patent No. 6706484; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 65
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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Best Local Similarity 83.33
Matches 100; Conservative
                                                                        Washington
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STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
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60 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRANGE: PETENT PC SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
PILING DATE: 14-Jan-2000
PRICING DATE: 18-FEB-1998
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.7%; Score 500; DB 2; Length 119; Best Local Similarity 83.3%; Pred. No. 4.6e-42; Matches 100; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ge, Liming
Moroney, Simon
Plueckthun, Andreas
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION DATE: 18-REB-1998

FILING DATE: 18-REB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPAX: (212)596-9000

INFORMATION FOR SEQ 1D NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jr., Esq.
Americas
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REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECTLE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
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of the
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Patent No. 6706484;
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Ilag, Vic
Ge, Liming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: James F.
STREET: 1251 Avenue
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US-09-490-324-65
  US-09-490-324-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119
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                                                                                                                                                                                                                                                                                                                                                   QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
                                                                                                                                                                                                                                                                                    Gaps
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ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk COMPATIEN FO COMPATIEN IBM PC COMPATIEN SYSTEM PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                               Length 119;
                                                                                                                                                                                                                                                                                    12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                           Score 500; DB 2;
Pred. No. 4.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-3an-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 39, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                           79.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                  Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-09-490-324-39
                                                                                                                                                                                                     US-09-490-153-65
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61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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                                                                                                                                                29
                                                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIXYSGSTNY
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                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ge. Liming
Ge. Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1213 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
     Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 119;
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Pred. No. 4.6e-42;
4; Mismatches 12.
  Score 500; DB 2;
Pred. No. 4.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/S TELECOMMUNICATION INFORMATION:
TELEFHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; ; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 65: US-09-490-324-65
                                                                                                                                                                                                                                                                                                                                                                     Sequence 65, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
  79.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York COUNTRY: USA
Query Match
Best Local Similarity
Matches 100; Conserv
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61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGD-GFDYWGQGTLVTVSS 117

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60 YKPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCAR-----YGRVFFDYWGQG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 QVQLQESGPGLVKPSETLSLTCAVSGSITSGGYYWSWIRQPPGKGLEWIGYIYYSGSTL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSETLSLTCTVSGYSIT-GGYLWNWIRQPPGKGLEWIGYISYDGTNN
                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Baughn, Mariah R.
TILLEOR INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORPUTER: 15M COMPACTION:
OPERATING SYSTEM: DOS
SOFTWARE: FASTEEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILLING DATE: HEREWITH
CLASSIPICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CEFTONE, MICHAEL:
REFERENCE/DOCKET NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                     Sequence 4, Application US/09049672A Patent No. 6135941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 650-855-059
TELEFAX: 650-845-4166
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANCTUT01
CLONE: 1513264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 TLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 TLVTVSS 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-049-672A-4
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60 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGLEWIGSIYHSGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVXPSETLSLTCTVSGYSI - TGGYLWNWIRQPPGKGLEWIGYISYDGTNN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 YKPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYMGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARGKWSKFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSBTLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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77.7%; Score 487; DB 2; Length 117;
Best Local Similarity 83.1%; Pred. No. 8.6e-41;
Matches 98; Conservative 4; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 497; DB 2; Length 117;
Pred. No. 8.8e-42;
3; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/10330613A
; Sequence 13, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE WUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT PELLOATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
LENGTH: 117
                                                                                                                                                                                                                                                APPLICANT: Williams, Andrew J
APPLICANT: Tempest, Philip R
APPLICANT: Holtet, Thor L
APPLICANT: Holtet, Thor L
APPLICANT: Holtet, Thor L
APPLICANT: Holten
APPLICANT: Dackson, Helen
APPLICANT: Daramola, Olalekan
APPLICANT: Daramola, Olalekan
APPLICANTION: Improvements relating to antibodies
FILE REFERENCE: AHB/CP5775333
CURRENT APPLICATION NUMBER: US/09/720,493
CURRENT APPLICATION NUMBER: GB 9814383.7
PRIOR FILING DATE: 1998-07-02
                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology Limited
                                                                                                                                                    Sequence 2, Application US/09720493
Patent No. 6827925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.3%;
Best Local Similarity 82.9%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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US-09-720-493-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCAR--YGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 486; DB 1; Length 123;
Pred. No. 1.1e-40;
                                                                                                APPLICANT: SATOCHIYA, Masayuki
APPLICANT: SATOC, Koh
APPLICANT: SATOC, Koh
APPLICANT: BENDIG, MATY
APPLICANT: BENDIG, MATY
APPLICANT: BENDIG, MATY
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER: IBM PC compatible
OPERATION TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: 25-258
FRING PARE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: MEGNER, HAGOLG,
RECISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
                                      Sequence 64, Application US/08137117D Patent No. 5795965
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 53.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 904136
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 123 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 77.5
Best Local Similarity 77.3
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-137-117D-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
RESULT 12
US-08-137-117D-64
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US-08-436-717-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
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Sequence 64, Application US/08436717 Patent No. 5817790 GENERAL INFORMATION: APPLICANT: TSUCHIYA, Masayuki

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1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 QVQLQESGPGLVRPSQTLSLTCTVSGYSITSDHAMSWVRQPPGRGLEWIGYISYSGITTX
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APPLICANT: BENDÍG, Mary
APPLICANT: JONES, Steven
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: RESHARED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADRESSS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Mashington
                                                                                                                                                                                                                                                                                                      CUUNTER: USA

ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: CI-OPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE: 24-APR: 1993
APPLICATION NUMBER: US/08/137,117
FILING DATE: 24-APR: 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR: 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR: 1991
ATYONEY/AGENT INFORMATION:
NAME: WEGNER, HAROH C:
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET UNMBER: 25,258
REGISTRATION NUMBER: 25,258
REFERENCE/OFFUTION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
RELEPANCE: (202) 672-5399
TELEFEXX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Mismatches
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Patent NO. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, JOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 77.39
Matches 92; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                       STATE: D.C
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US-08-137-117D-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 NPSLKSRVTMLRDTSKNOPSLRLSSVTAADTAVYYCARSLARTTAMDYWGQGSLVTVSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCAR--YGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Sequence 69, Application US/08436717
Fatent No. 5817790
GENERAL INFORMATION:
APPLICANT: SAUCHIYA, Masayuki
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: SALDARHA, Jose
ITILE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
ITILE OF INVENTION: INTERLEUKIN-6 RECEPTOR
CORRESPONDENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
RESHAPED HUMAN ANTIBODY TO HUMAN INTERLEUKIN-6 RECEPTOR: 158
                                                                                       ADDRESSER: FOUNTE ADDRESS:
ADDRESSER: FOLSY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURSTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-ARR-1992
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 25-ARR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HAROLD C.
REGISTRATION NUMBER: 25,258
REFERENCE/POCKET NUMBER: 25,258
REFERENCE/POCKET NUMBER: 53466/126/AAOK
TELEPHONE: (202)672-5399
TELLEFAN: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 138 amino acide
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 77.5
Best Local Similarity 77.3
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-137-117D-69
TITLE OF INVENTION: RE. TITLE OF INVENTION: IN. NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-436-717-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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20 QVQLQESGPGLVRPSQTLSLTCTVSGYSITSDHAMSWVRQPPGRGLEWIGYISYSGITTY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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7
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COUNTEY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE: 24-APR-1993
APPLICATION NUMBER: US/08/137,117
FILING DATE: 24-APR-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-PEB-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 15-PEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HARCH Z.
REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: January 10, 2006, 20:58:05 Job time : 23.847 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904136
INFORMATION FOR ESQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 77.33
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-436-717-69
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Wed Jan 11

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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OM protein - protein search, using sw model

January 10, 2006, 20:28:02; Search time 14.1157 Seconds (without alignments) 797.508 Million cell updates/sec Run on:

US-10-735-916A-79 627 1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	g variable region	heavy cha	chain	heavy chain	heavy	heavy	Ig heavy chain V	Ig heavy chain	heavy	Ig heavy chain	Ig heavy	Ig heavy	Ig heavy chain	Ig heavy	Ig heavy	Ig heavy chain	Ig heavy chain	Ig heavy	Ig heavy chain	Ig heavy cha	lyh	Ig heavy cha	Ig heavy						
50	Ð	137782	831690	830530	813519	S24443	831511	S30534	S31586	S44114	\$31512	878052	878055	837200	844113	A49045	807637	878051	AVMS35	838718	831676	S09711	S47010	128195	S20780	E25114	A24770	A26340	C53285	
	DB	2	7	~	7	7	7	~	~	~	~	N	~	~	~	~	~	~	Н	N	7	~	N	~	~	~	7	~	~	•
	Query Match Length	140	130	123	147	118	155	130	139	129	155	140	145	121	121	140	136	135	137	116	137	146	126	117	118	119	140	118	119	•
de	Query .Match	81.2	78.8	76.7	76.2	74.9	74.6	73.9	73.9	73.8	73.7	73.6	73.3	73.0	72.9	72.7	72.6	72.6	72.4	72.3	72.2	72.1	71.9	71.8	71.4	71.3	71.1	70.1	70.0	
		509	494	481	478	469.5	468	463.5	463.5	462.5	462	461.5	459.5	458	457	456	455.5	455	454	453.5	452.5	452	450.5	450	447.5	447	446	439.5	439	
		-	~	m	4	ហ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	1

Ig heavy chain V r Ig heavy chain V r	heavy	ig neavy chain pre Ig heavy chain V r Ig lambda chain V	heavy chain heavy chain	heavy chain heavy chain	Ig heavy chain y r Ig heavy chain pre Ig heavy chain V r	heavy chain heavy chain
S12421 S54906	S31696 S30752	824672 S26906 S4125	PL0100 S30529	B26340 S26902	S19668 A41287 S12416	A25114 F25114
0.0	000	7 77 77	0 0	~ ~ ~	200	0.00
98 134	139	134 97 105	135	116	127 139 97	120
69 9.69	69.9	69.9 69.3 9.3	69.3	69.1	69.0	68.7
438 438	438	434.5 434.5 534.5	434.5	433.5	432.5 431.5	430.5
30 31	332	 	37 38	0 4 0 0	4 4 4 1 2 4	44

## ALIGNMENTS

RESULT 1

	137782
_	Ig variable region (VDJ) (clone T23-9) - human (fragment)
	C.Species: Homo sapiens (man)
_	C;Date: 16-Feb-1996 #sequence revision 13-Mar-1997 #text_change 23-Jul-1999
_	C;Accession: 137782; S25476
_	R; Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
_	Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
_	A,Title: Somatic diversification in the heavy chain variable region genes expressed by I
	A; Reference number: A36876; MUID: 94119917; PMID: 8290556
	A;Accession: 137782
	A;Status: preliminary
	A; Molecule type: mRNA
	A; Residues: 1-140 < RES>
	A, Cross-references: UNIPARC: UP10000176E83; EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PII
	C; Superfamily: immunoglobulin V region; immunoglobulin homology
	F;46-128/Domain: immunoqlobulin homology <1MM>

Gaps 8 Query Match 81.2%; Score 509; DB 2; Length 140; Best Local Similarity 82.9%; Pred. No. 1.9e-39; Matches 102; Conservative 4; Mismatches 9; Indels

3, 61 KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCAR-----YGRVFFDYWGQGTLVT 114 78 9 20 QVQLQESGFGLVKPSETLSLICTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIXYSGSTNY 1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 138 VSS 140 115 VSS 117 셤 ò 셤 Š ò 셤

RESULT 2
S1850
Ig heavy chain V region - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: 831690
R; Cuishiner, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human immunoglobulin diversity operate from the A; Reference number: 831690
A; Accession: 831690
A; Statuus: preliminary
A; Molecule type: mRNA
A; Residues: 1-130 <CUI.
A; Cross-references: UNIPARC: UPI0000116471; EMBL: Z14199; NID: g30984; PIDN: CAA78568.1; PII
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin

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Score 478; DB 2;
Pred. No. 1.4e-36;
5; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
    76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 74.9%;
1 Similarity 79.0%;
94; Conservative 6
                                              Conservative
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Matches 94; Conserv
                         Similarity
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                       Best Local Simi
Matches 97;
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      Query Match
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19 heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S13519
R;Mortari, F; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked A;Reference number: S13519
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked A;Reference number: S13519
A;Accession: S13519
A;Accession: S13519
A;Accession: S13519
A;Residues: 1-147 cAMOR>
A;Residues: 1-147 cAMOR>
A;Crosa-references: UNIPARC:UPI0000115EB5; EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PIC C;Reywords: heterotestramer; immunoglobulin
C;Superfeamily: immunoglobulin
F;41-125/Domain: immunoglobulin
                                                                                                                                                                                                                             61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCAR-----YGRV--FFDYWGQGT 111
                                                                                                                                                                                                                                                       61 NPSLKSRVTISVDTSKNOPSLOLRSVTAADTAVYYCAR-GRYCSSTSCNWFDPWGGGTLV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGYSISSGYYWGWIRQPPGKGLEWIGSMFHSGSSYY 60
                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Homo sapiens (man)
Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
Accession: S30530
                                                                                                                                                                   QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWSRQPPGKGLEWIGYIYYSGSTNY
                                                                                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                             10;
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C; Date: 03-Mar-1994 # Heequence_revision 10-Nov-1995 #text_change 16-3
C; Date: 03-Mar-1994 # Heequence_revision 10-Nov-1995 #text_change 16-3
C; Accession: S30530
A; Reference number: S30520
A; Reference number: S30530
A; Accession: S30530
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-123 < AMA>
A; Residues: 1-123 < AMA>
A; Cross-references: UNIPARC:UP10000176C83; EMBL:Z18316
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
                                            Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 123;
                                              Score 494; DB 2; Length 13
Pred. No. 4.1e-38;
6; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.7%; Score 481; DB 2; Length 12 ilarity 77.4%; Pred. No. 6e-37; Conservative 7; Mismatches 13; Indels
  F;20-102/Domain: immunoglobulin homology <IMM>
                                              Query Match 78.8%;
Best Local Similarity 78.6%;
Matches 99; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region - human
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Best Local S:
Matches 96
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A,Cross-references: UNIPARC:UP10000115FB9; EMBL:X61650; NID:g37720; PIDN:CAA43831.1; PID R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. 222, 581-597, 1991
A,Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph A;Reference number: S19663; MUID:92085276; PMID:1748994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31511
S;Chategapor, P.; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AjStatus: preliminary
AjActus: mRNA
AjMolecule type: mRNA
AjRosidues: 1-155 <CHA>
AjCross-references: UNIPARC:UP100001160FF; EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID
Cj.Superfamily: immunoglobulin V region; immunoglobulin homology
Cj.Keywords: heterotetramer; immunoglobulin homology <IMM>
Fj47-129/pomain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                          60 YKPSLKDRVTISRDTSKNOPSLKLSSVTAADTAVYYCAR----YGRVPFDYWGQGTLVTV 115
                                                                                                                                                                                                                                                                                                                                    87 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARPLLWFGEL-FDYWGGGTLVTV 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region (VH4DJ) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S24443; S19667
K;Jones, P.T.
submitted to the EMBL Data Library, October 1991
                                                                                                                                             1 QVQLQESGPGLVKPSETLSLTCTVSGYSI-TGGYLWNWIRQPPGKGLEWIGYISYDGTNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSETLSLVCTVSGGSLSFSY-WGWIRQPPGKGLEWIGYISHRGSTDY
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Length 147;
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A;Cross-references: UNIPARC:UPI0000176B52; EMBL:X61650
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heteroretramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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Pred. No. 6.4e-36;
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44114
E;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: UNIPARC:UP10000116639; EMBL:231579; NID:g472968; PIDN:CAA83451.1; PI C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31512
R;Chastegner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A;Reference number: S31509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UP100001160F9; EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PIDC;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                            61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVF-----FDYWGQGTLV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NPSFKSRVTISADTSKNOFSLKVNSVTAADTAVYXCARRNYDFWSGGDGPFDYWGQGTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWWSWVRQPPGKGLEWIGEIYHSGSTNY
                                                                                                                         20 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPAGKGLEWIGRIYTSGSTNY
                                                                                                                                                                                                            61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYG----RVFFDYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 OVOLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                   1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                         5;
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                         Indels
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Pred. No. 3e-35;
7; Mismatches 19;
Pred. No. 2.7e-35;
                            5; Mismatches
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73.4%;
78.5%;
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Best Local Similarity 73.4%
Best Local Similarity 73.4%
                               95; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-129 <HAW>
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A,Molecule type: mRNA
A,Residues: 1-155 <CHA>
Best Local Similarity
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                            Matches
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31586
C;Accession: S31586
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Abscription: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585
A;Accession: S31586
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-139 < CUNIPARC;UPI000011646E; EMBL:Z14196; NID:g30978; PIDN:CAA78565.1;
A;Cross-references: UNIPARC;UPI00011646E; EMBL:Z14196; NID:g30978; PIDN:CAA78565.1;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                            61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRV--FFDY-----WGQGTLV 113
                                                                                                                                                                                                                                                                                                            92 NPPLKSRVTISVDTSKNOFSLKVSSVTAADTAVYYCARGGGISSWYDYYGMDVWGQGTTV 151
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31586
                                                                                                                                                                                         33 QVQLQESGFGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPFGKGLEWIGYIXYTGSATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGSYYWSWIRQPAGKGLEWIGRIYTSGSTW
                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                         Gaps
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                                                                                            8;
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                                   Length 155;
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                                                                                            14; Indels
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Pred. No. 2.5e-35;
5; Mismatches 17;
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                               74.6%; Score 468; DB 2; 76.6%; Pred. No. 1.2e-35; ive 7; Mismatches 14;
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Best Local Similarity 73.1%;
Matches 95; Conservative
                                                               Local Similarity 76.6
nes 95; Conservative
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GOGTMVTVSS 130
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                                      Query Match
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R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
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A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sydox chain precursor V-D-J region (clone mAB 63VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78052; S23717
R;Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78052
A;Molecule type: mRNA
A;Residues: 1-140 cHAR>
A;Residues: 1-140 cHAR>
A;Residues: UNIPARC:UPI0000115E89; EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h patient.
A;Residues: 15-111 cHAW>
A;Molecule type: mRNA
A;Residues: 15-111 cHAW>
A;Accession: S23717
A;Molecule type: mRNA
A;Residues: 15-111 cHAW>
A;Cross-references: UNIPARC:UPI0000116417; EMBL:X54441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin (fragment) #status predicted cSIG>
F;1-14/Domain: signal sequence (fragment) #status predicted cANT>
F;29-111/Domain: immunoglobulin homology cIMM>
F;20-111/Domain: im
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C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: 878055, 823720
R;Harindranath, N.
Ribarindranath, N.
Reference number: 878051
A;Reference number: 878055
A;Accession: 878055
A;Cross-references: UNIPARC:UPIO00011558C; EMBL:X54445; NID:g37817; PIDN:CAA38312.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
      ä
                                                                                                                                                                                                     KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVF-----FDYWGQGTLV 113
                                                                                                                                                                                                                                              61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVF------FDYWGQG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                     91
                                                                                                         QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYMSWIRQPPGKGLEWIGYIYYTGSATY
                                                                       QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Сарв
   8; Gaps
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      6; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.6%; Score 461.5; DB 2; Best Local Similarity 73.2%; Pred. No. 4.1e-35; Matches 93; Conservative 7; Mismatches 16;
      93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 TLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLVTVSS 140
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      Matches
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Int. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: UNIPARC: UP100001161AC; EMBL: X74587; NID: 9402639; PID: 9402640 C; Superfamily: immunoglobulin V region; immunoglobulin homology < IMM> F; 15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCAR-----YGR-VFFDYWGQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYGRV----FFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Bacession: S37200
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F. submitted to the EMBL Data Library, August 1993
A;Description: Production and cloning of TMV-specific monoclonal antibodies.
A;Reference number: S37200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWWSWVRQPPGKGLEWIGBIYHSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 OVOLOESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIROPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                    F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>F:18-145/Product: Ig heavy chain (fragment) #status predicted <MAT>F:32-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 18-115 < HAM>
A; Residues: 18-115 < HAM>
A; Cross-references: UNIPARC: UDI00001769D2; EMBL: X54445
A; Note: the authors translated the codon GCA for residue 67 as Arg
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                   patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.3%; Score 459.5; DB 2; ilarity 72.7%; Pred. No. 6.5e-35; Conservative 6; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.0%; Score 458; DB 2; I larity 71.7%; Pred. No. 7.3e-35; Conservative 13; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 GTLVTVSS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 GTLVTVSS 117
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nes 93; Conserv
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Matches 86: Conser
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Useay Lucas, Luc
                              A;Accession: S44112
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-121 <HAW)
A;Cross-references: UNIPARC: UPIO00011662F; EMBL: 231389; NID: 9472967; PIDN: CAA83264.1; PI
A;Cross-references: UNIPARC: UPIO00011662F; EMBL: 231389; NID: 9472967; PIDN: CAA83264.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
F;15-99/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 YKPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVF---FDYWGQGTLVTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQBSGPGLVKPSETLSLTCTVSGGYISSSSYYWGWTRQPPGKGLEWIGSIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVS-GYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J heavy chain V region (anti-B cell autoantibody) - human (fragment) Species: Homo sapiens (man) Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLMNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 457; DB 2; Length 121;
Pred. No. 9e-35;
5; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 72.7%; Score 456; DB 2; Length 140; Best Local Similarity 75.4%; Pred. No. 1.3e-34; Matches 92; Conservative 7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: January 10, 2006, 20:55:15
Job time : 14.1157 secs
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 72.9%;
Best Local Similarity 75.2%;
Matches 91; Conservative
Reference number: S44105
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=2511001;
Sanz I., Kelly P., Williams C., Scholl S., Tucker P., Capra J.D.,
"The smaller human VH gene families display remarkably little
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in rheumatic carditis and normal
Q510j1
Q53vg9
Q53vg9
Q510l9
Q510l9
Q53vz
Q53vz
Q50l9
Q90l75
Q723y6
Q723y6
Q723y6
Q60xx7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1] MULTINESTED SEQUENCE.
NUCLECTIDE SEQUENCE.
NUCLINE-98277139; PubMed-9614934; DOI=10.1006/clin.1998.4531;
NU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diamond B.;
"Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.";

Exp. Med. 174:1639-1652(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13219 MW; 1BDB86B6420EA0BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                             119 AA
0510J1_RAT
053VR6_MOUSE
HV2G_HÜMAN
0510J9_RAT
053VR2_MOUSE
059M839_RAT
053W2_MOUSE
UV2F_HÜMAN
09UL75_HÜMAN
07273Y6_HUMAN
1747_MOUSE
06MZX7_HUMAN
                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                  Q6MZX7_HUMAN
Q8TC63_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymorphism.";
EMBO J. 8:3741.3748(1989).
EMBL, AR056277.1; -; mRNA.
PIR; PH0875; PH0876.
PIR; S12416; S12416.
HSSP, OP1820; IG70.
SMR; Q9UJ73; 1-119.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
INTERPOSTIE; PS50835; IG_LIKE; 1.
NON TER
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NON TER
SEQUENCE 119 AA; 13219 MW; IBDB86B
                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Q9UL73;
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Best Local Similarity 80.0
Matches 96; Conservative
477
1199
1199
1198
469
198
192
1129
1116
476
476
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   664.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment).
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rattus norv
homo sapien
mus musculu
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                                                                                                                          January 10, 2006, 20:26:41 ; Search time 78.8731 Seconds (without alignments) 1046.577 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSETLSL.....RYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
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009gm20
006gmx7
006lbd5
006lbd5
005973
005973
005374
0053745
0056x8
0053747
0056x8
005080
005901
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Q8izd7
Q6nyh3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9u173
                    GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                          2166443 segs, 705528306 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           053V25_MOUSE
072374_HUMAN
085X22_HUMAN
086SX2_HUMAN
096KX8_HUMAN
056KX8_HUMAN
056XX8_HUMAN
055XV7_MOUSE
053VQ1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        056996_RAT
056998_RAT
HV2I HUMAN
0530X3_MOUSE
08WUX4_HUMAN
098U10_HUMAN
06GMX5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          095973_HUMAN
Q6P418_HUMAN
HV46_MÕUSE
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Q81ZD7 HUMAN
Q6NYH3 HUMAN
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OGGMX7_HUMAN
OGLBQS_MOUSE
QSU413_MOUSE
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HV60 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                           OM protein - protein search, using sw model
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Q6P4I8
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                                     length: 0
length: 2000000000
                                                                                                                                                                                               US-10-735-916A-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
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Minimum DB Maximum DB

Database :

Result

Perfect score:

Run on:

Sequence:

Scoring table:

7

Gaps

4

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20 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-GYYWSWIRQPAGKGLEWIGRIYTSGSTNY 78
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METARUBERG R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MISCHALL S.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Diatchenco L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu K., Gibbs R.A.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Raha Resley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rotiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Bromeration and initial analysis of more than 15,000 full-length human
                                                                                                                                                   119
  9
                                                 59
                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                               QVQLQESGPGLVKPSETLSLTCTVSGGSIC-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
                                                                                                                         QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                    61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCAR---YGRVFFDYWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 465;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073766; AAH73766.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                               465 AA.
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                             PRT;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig.MHC.
InterPro; IPR003596; Ig.v.
Pfam; PP07654; Cl-set; 3.
                                                                                                                                                                                                                                                                        QĞGMX6 HUMAN PRELIMINARY;
Q6GMX6;
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SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
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TISSUE-Primary B-Cells;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months old;

MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.D., Collins F.S., Wagner L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Alschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Undin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerthield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerthield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerthield Y. Schein J.E., Jones S.J.M., Marra M.A.,

Schnerthield Y. Schein J.E.,

Schnerthield Y. Schein J.E.,

Scholethield Y. Schein J.E.,

Scholethield Y. Schein 
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61 KPSLKORVTISRDISKNOFSLKLSSVTAADTAVYYCARYGRVFPDYWGQGTLVTVSS 117
                                                                                            19 NPSLKSRVTMSVDTSKNOFSLKLSSVTAADTAVYYCARGRFTYFDYWGQGTLVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VOLOESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC002091; AAH02091.1; -; mRNA. HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogiobulin domain.
SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 75.1%; Score 471; DB 2; Local Similarity 74.1%; Pred. No. 2.4e-40; les 86; Conservative 14; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0003823; F:antigen binding; IEA
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; Pr07654; C1-eet; Z.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                Q99M22_MOUSE PRELIMINARY;
Q99M22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOC238447 protein.
Name=LOC238447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Mix FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Mix FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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QGGMX7 HUMAN PRELIMINARY;
QGGMX7;
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Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
Homo sapiens (Human).
                                                                                                                      111 TLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                                                                                                                                                          140 TMVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
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                                                                                                                                                                                                                                                                                                             5
HUMAN
                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                       SOW REPRESENTATION OF THE PROPERTY PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGG-YLWNWIRQPPGKGLEWIGYISYDGTNN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQPPGKGLEWIGYIYYSGSTY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                           13; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Straugherg R.; Straugherg R.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC073773; AAH73773.1; -: menhyane: IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52286 MW; 622AABA5C62DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                             476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC073773; AAH73773.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INCEPPO, IPRO01359; IG.
INTERPO, IPR00110; IG-11ke.
INTERPO, IPR00110; IG-11ke.
INTERPO, IPR00359; IG_C1.
INTERPO, IPR00359; IG_C1.
INTERPO, IPR00359; IG_V.
INTERPO, IPR00359; IG_V.
INTERPO, IGC1, IG_V.
INTERPO, IGC1, IGC1
                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                     OGGMX1_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                     62
                                                                                                                                                                                                                                                                                                                                                   OGGMX1;
                                                                                                                                                                                                                                                                          Q6GMX1
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RN NUCLEOTIDE SEQUENCE.

RX Strausberg N.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Causiner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Alusiner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Alusiner R.D., Marvisina K., Parmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marvisina K., Parmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marvisina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Whiting M., Madan J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

RA "Generation and initial analysis of more than 15,000 full-length human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                          Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.8%; Score 462.5; DB 2; Length 477; 77.5%; Pred. No. 1.8e-39; ive 9; Mismatches 13; Indels 5.
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EMBL; BC073765; AAH73765.1; -; mRNA.
SWR; Q6GWX7; 247-455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 477 AA; 51631 MW; 9FES9C09C50CFF85 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Matches
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                                                                                    61 KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVF---FDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 VQLQESGPGLVKPSQSLSLTCSVTDPSITSGYYWHWIRQFPGNKLEWMGYISYDGSNGYN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 PSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCAR-YGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQTAGKGLEWIGYISHSGSTTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

Muroidea; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEDLINE-90067954 PubMed=2587273;
Urakov D.N., Deev S.M., Polyanovsky O.L.;
Urakov D.N., Deev S.M., Polyanovsky O.L.;
"The structure of the expressible VH gene from a hybridoma producing monoclonal antibodies against porcine transferrin.";
Nucleic Acida Res. 17:94811989).
EMBL; X1674; CAB34714.1; -; Genomic_DNA.
HSSP; P18532; IKCV.
HSSP; P18532; IKCV.
INTERPRO; IPR003599; IG.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR00409; IG; 1.
SMART; SM00409; IG; 1.
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STRAIN=FVB/N; TISSUE=Colon;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) VH gene product (Fragment).
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                              136 AA
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QGLBQS;
05-JUL-2004 (TrEMBLrel. 27,
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QSU413;
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Name=LOC544903;
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

A staplaton M., Soares M.B., Bonaldo M.F., Caraninci P., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McDwan P.J., McKernan K.J., Malek J.A., Gunzatne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman M., Madan B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Rodriguez A.C., Grimwood S.J.M., Marra M.A.;

Roberztion and initial analysis of more than 15,000 full-length human
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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"Clonal proliferation of IgM secreting B cell in the synovium of Behcer's patient with arthritis.";
Bubitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
[2]
NUCLEOTIDE SEQUENCE.
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EMBL, BC00312; AAH85312.1; -; mRNA.

GO, GO:000312; F:antigen binding; IEA.

InterPro; IPR003199; Ig.

InterPro; IPR003106; Ig.-1ike.

SWART; SW00409; IG: 3.

SWART; SW00407; IGC: 1; 3.

SWART; SW00407; IGC: 1; 3.

SWART; SW00409; IG INKC; UNKNOWN 2.

SPROSITE; PS00396; IG MHC; UNKNOWN 2.

SRQUENCE 483 AA; 52714 MW; 7C272DASO1A4AOD1 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
VH4 heavy chain variable region precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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STRAIN=FVB/N; TISSUE=Colon;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.
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HV46_MOUSE
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                                                                                                                                                                                                          20 QLQLQESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPEKGLEWIGSLHNSGSDY 79
                                                                                                                                                                                                                                       60 YKPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
      Harindranath N., Goldfarb I.S., Ikemateu H., Burastero S.E., Wilder R.L., Notkins A.L., Casali P., "Complete sequence of the genes encoding the VH and VL regions of low-and high-affinity monoclonal IgM and IgAl rheumatoid factors produced by CD5+ B cells from a rheumatoid arthritis patient."; Int. Immunol. 3:865-875(1991). EMBL: AF103795; AAC79084.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                    Gaps
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                                                                                                                                                                    DB 2; Length 150;
                                                                                                                                      VH4 heavy chain variable region.
                                                                                                                                                                           75.4%; Pred. No. 3.35-33,
tive 9; Mismatches 19; Indels
                                                                                                                                                     150 AA; 16315 MW; 85664E04938AA7C9 CRC64;
                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                    72.5%; Score 454.5; DB 2 75.4%; Pred. No. 3.5e-39;
                                                                                                                              Potential.
                                                                                                                                                                                                                                                                                                   Created)
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                                                          PIR, S11673, S31673.
PIR, S11673, S31673.
PIR, S78056, S78056.
HSSP, P01820; 1G7J.
SMR, OSS973, 20-147.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-v.
SMART; SM00406, IG-v; I.
PROSITE; PS50835; IG_LIKE; I.
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Q6P418;
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                                                                                                                                                                                                                                                                                                                         IGHD protein.
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61 KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIJINE-89238351; PubMed-2497341; DOI=10.1016/0161-5890(89)90133-8; Rinfret A., Horne C., Dorrington K.J., Klein M.; "Cloning, sequencing and expression of the rearranged MOPC 315 VH gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWMSWVRQPPGKGLEWIGEIYHSGSTNY
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"Structure and function of immunoglobulin genes and precursors.";
Fed. Proc. 38:1839-1845(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 576;
                                                                                                                                                                                                                                                               InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003006; IG.—II.
InterPro; IPR003006; IG—II.
InterPro; IPR003596; IG.—II.
InterPro; IPR003596; IG.—II.
InterPro; IPR003596; IG.—II.
InterPro; IPR00409; IG. II.
InterPro; IPR00409; IG. II.
InterPro; IPR00409; IG. II.
InterPro; IPR00409; IG. II.
InterPro; IPR04178; IG. III.
IPR04178; IPR041
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                                  Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063184; AAH63184.1; -; mRNA.
HSSP; P01820; 1A7N.
Ensembl; ENSG0000196122; Homo sapiens.
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Pred. No. 1.6e-38;
8; Mismatches 20
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01-AUG-1992 (Rel. 23, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 AA
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MEDLINE=78094475; PubMed=414225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Immunol. 26:431-434(1989).
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TISSUE=Primary B-Cells;
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                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                   MEDLINE=77244979; PubMed=268248;
Hood L., Margolies M.N., Givol D., Zakut R.;
Unpublished results, cited by:
Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
-!- MISCELLANEOUS: This alpha chain was isolated from a myeloma protein that has anti-dinitrophenyl activity.
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                                                                                                                                                                                                                                                                                                     chain V region MOPC 315.
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G -> GG (in Ref. 1; CAA30727).
G -> H (in Ref. 2).
Gy -> YG (in Ref. 4).
N -> D (in Ref. 4).
Missing (in Ref. 4).
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mouse myeloma protein with anti-hapten activity.";
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                                                                                                                                                                                                                                                     SMART; SM00406; IGV; 1.—
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Signal.
          Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974)
                                                                                                                                                                        EMBL; M27638; AAA61337.1; -; Genomic_DNA.
EMBL; X07880; CAA37727.1; -; Genomic_DNA.
PIF; PL0102; AVMS35.
HSSP; P01820; 1G7J.
SMR; P01822; 20-137.
Ensembl; EMSNUSGO000057048; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR00710; Ig-like.
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Matches 84; Conservative
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Homo sapiens (Human). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,

Last sequence update) Last annotation update)

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01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,

IGHM protein. Name=IGHM;

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Neale GA., Kitchingman G.R.;
Neale GA., Kitchingman G.R.;
mRNA transcribe initiating within the human immunoglobulin mu heavy chain enhancer region contain a non-translatable exon and are extremely heterogeneous at the 5' end.";
Nucleic Acids Res. 19:2427-2433(1991).
EMBL; BC011857; AAH1857.2; -; mRNA.
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InterPro; IPR003110; Ig-like.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig-d.:
InterPro; IPR003596; Ig-w.
Pfam; PR07654; Cl-set; 4.
SMART; SM00400; IG; 2.
SMART; SM00400; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00399; IG MHC; UNCNOWN 3.
SEQUENCE 620 AA; 68125 MW; 990AlA4A6E8FF27B CRC64;
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SWR; Q96EY0; 27-251.
Ensembl; ENSG00000130076; Homo sapiens.
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Matches 93; Conservative
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NIH MGC Project;
                                   rissum=Primary B-Cells;
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NUCLEOTIDE SEQUENCE
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.

TISSUE=Human rectum tumor;

TISSUE=Human rectum tumor;

A Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

R Bloecker H., Boecher M., Miemann S.;

L Submitted (JUN-2003) to the EWBL/GenBank/DDBJ databases.

E RMEL, EX538066; CAD97996.1; -; mRNA.

R RSP; P01820; 1G7J.

R RSP; Q72379; 248-456.

R RISSEMDI, ENSGON000130076; Homo sapiens.

R InterPro; IPR00310; IG-1.

R InterPro; IPR00310; IG-1.

R InterPro; IPR03597; IG-1.

R InterPro; IPR03596; IG-1.

R InterPro; IPR03596; IG-1.

R InterPro; IPR03596; IG-1.

R Pfam; PF07654; C1-set; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases
EMBL; X03378; CAA27095.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 AA; 13931 MW; 502E51A5213F056E CRC64;
                                                                                                                                                                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
VH-D-JH region (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OT2379 HUMAN PRELIMINARY; PRT; 478 AA. 072379. 01-0CT-2003 (TrEMBLrel. 25, Created) 01-0CT-2003 (TrEMBLrel. 25, Last sequence update) 01-0MR-2004 (TrEMBLrel. 26, Last annotation update) Name-DFESD686K04218 (Fragment). Name-DFESD686K04218; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 71.3%; Score 447; DB 2; Il Similarity 70.3%; Pred. No. 1.6e-38; 83; Conservative 14; Mismatches 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE OF 28-29.
                                                                                                Q53VQ5_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                RESULT 12
Q53VQ5 MOUSE
1D Q53VQ5 M
AC Q53VQ5 M
DT 13-SEP-2(
DT 13-SEP-2(
DT 13-SEP-2(
DT 13-SEP-2(
DT 13-SEP-2(
DT 13-SEP-2(
DE WH-D-JH 3
DE WH-D-JH
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60 YKPSLKDRVTISRDTSKNOPSLKLSSVTAADTAVYYCAR---YGRVFFDYWGQGTLVTVS 116
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2004 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKPZp686C0218 (Fragment).
Name-DKFZp686C02218;
Homo saplens (Human).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloecker H., Boecher M., Wiemann S.;
Submitted (JUN-2013) to the EMBL/GenBank/DDBJ databases.

RMBL; BX538077; CAD98001.1; -; mRNA.

RMSP; PO1820; 1G7J.

RMSP; PO1820; 1G7J.

RESEMBL; ENSG00000130076; Homo sapiens.

RICEPPO; IPR003596; 1g_MHC.

RICEPPO; IPR003596; 1g_MHC.

RICEPPO; IPR003596; 1g_MHC.

RESMART; SMO0406; 1GV; 1.

ROSITE; PS50835; 1G_LKE; 4.

ROSITE; PS50835; 1G_LKE; 4.

RMSPROSITE; PS00290; 1G_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                     19 QVQLQESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQAPGRGLEWMGYIYYSGSTY
                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGYS1-TGGYLWNWIRQPPGKGLEWIGYISYDGTNN
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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2
                                                                                                                                                                                             Length 478;
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                                                                                                                                                                                          Similarity 71.9%; Score 439.5; DB 2; Length Similarity 71.9%; Pred. No. 4.6e-37; 37; Conservative 14; Mismatches 15; Indels
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00230; IG_MHC; UNKNOWN_2.
Hypothetical protein.
1 1 1 1 SEQÜENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
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                                                                                                                                                                                                                       Local Similarity
nes 87; Conservative
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Q7Z374;
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||| 150 VSS 152

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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone GSODD004YM19 of B cells (Ramos cell line) of Homo sapiens (Human) (Fragment).
Homo sapiens (Human)
Example (Human)
Full-sapiens (Huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 69.3%; Score 434.5; DB 2; Length 139; Best Local Similarity 86.7%; Pred. No. 3.9e-37; Matches 85; Conservative 3; Mismatches 9; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX248300; CAD62627.1; -; mRNA.
HSSP; PO1820; 1G7J.
SNR; Q86SX2; 33-129.
Ensembl; ENSGG0000130076; Homo sapiens.
InterPro; IPR007110; 1g-1ike.
InterPro; IPR00710; 1g-1ike.
SNART; SM00406; IGV; 1.
PROSITE; PSS0835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
TISSUEs calls:
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;
                                                                                                                                                   139 AA
                                                                                                                                                   PRT;
                                                                                                                                            Q86SX2_HUMAN PRELIMINARY;
Q86SX2;
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TISSUE=B cells;
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NCBL_TaxID=9606;
                                                                                    HUMAN
RESULT 15
0865XZ HUM
10 0066XX
AC 0865X
AC 0865X
AC 0865X
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DE RUII-
DE RUII-
DE RUII-
CO RUEAT
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92 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 129 Search completed: January 10, 2006, 20:53:27 Job time : 78.8731 secs

61 KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCAR 98

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Gaps

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January 10, 2006, 20:07:41; Search time 80.7649 Seconds (without alignments) 636.505 Million cell updates/sec
                                                                                                                                                                        1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117
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5.1.6
Compugen Ltd.
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 version 5
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Maximum Match 100%
Listing first 45 summaries
                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
 GenCore (c) 1993
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geneseqp20028:*
geneseqp2003a8:*
geneseqp2003b8:*
geneseqp20048:*
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geneseqp1990s:*
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length: 2000000000
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627
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	TENT THE CLOSE TO BE THE THE THE THE THE THE THE THE THE TH	٠.	-	Adj76915 Anti-IGF-	_	Adj76909 Anti-IGF-	_	Adj76911 Anti-IGF-	Adz67081 Human ant	Adj76917 Anti-IGF-	Adz67087 Human ant	Adj76919 Anti-IGF-	_	Adj76903 Anti-IGF-	_	Adj76886 Anti-IGF-	_	Adc27457 Humanised	Aay15126 Anti-muri	Adp03973 Murine-ex	Adc27455 Humanised	Ads16559 Human ant	Adc27459 Humanised	Adp03885 Murine-ex	Adp03889 Murine-ex
SUMMARIES	ID	AD 126012		ADZ67083	ADJ76915	ADZ67085	ADJ76909	ADZ67079	ADJ76911	ADZ67081	ADJ76917	ADZ67087	ADJ76919	ADZ67089	ADJ76903	ADZ67073	ADJ76886	ADZ67056	ADC27457	AAY15126	ADP03973	ADC27455	ADS16559	ADC27459	ADP03885	ADP03889
	DB	-	٠.	D	7	σ	7	σ	7	σ	7	σ	7	σ	7	σ	7	σ	,	m	7	7	80	^	7	7
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	% Query Match			100.0	100.0	100.0	99.4	99.4	99.4	99.4	98.1	98.1	98.1	98.1	86.3	86.3	86.3	86.3	84.0	81.3	80.9	80.8	80.8	80.3	80.3	80.3
	Score	693	770	627	627	627	623	623	623	623	615	615	615	615	541	541	541	541	526.5	509.5	507	506.5	506.5	503.5	503.5	503.5
	Result No.		4	7	м	4	ß	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of

Disclosure; SEQ ID NO 79; 164pp; French.

Adp03958 Murine-ex Adp03957 Murine-ex Abb07171 ebvHigM M Adi26658 Human ant		Ade28479 Human ant Ady74798 Human IgG Aay44615 Human ant Ade28491 Human ant Ade28471 Human ant	Aac30915 dI-NHS76 Aac30913 dI-NHS76 Aea21456 Human ant Adx98267 Human ant Ads16615 Human ant Ads16613 Human ant Ade28447 Human ant
ADP03958 ADP03957 ABB07171 ADI26658	ADF0388/ ADF03884 AAW27554 ABJ18676 ADE28455	ADE28479 ADY74798 AAY44615 ADE28491 ADE28471	AAO30915 AAO30913 AEA21456 ADX98267 ADS16505 ADS16613 ADE28447
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120	122 122 119 119	466 119 117 121 466	580 580 122 139 121 169
80.1 79.8 79.8	79.8 79.7 79.7 79.7	79.7 79.3 79.3	79.3 79.3 79.0 78.9 78.9
502.5 500.5 500.5	500 500 500 500 500	500 498 497 497	4997 4995.5 4995.5 494.5 494
25 27 28 28	332133	34 35 37 88	W 4 4 4 4 4 4 9 0 0 11 12 11 11 11 11 11 11 11 11 11 11 11

## ALIGNMENTS

insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR. New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers. cytostatic; antipsoriatic; antibody; (FABR ) FABRE MEDICAMENT SA PIERRE. ADJ76913 standard; protein; 117 AA. Anti-IGF-1R related protein #24. Leger O; 18-JAN-2002; 2002FR-00000653. 18-JAN-2002; 2002FR-00000654. 07-MAY-2002; 2002FR-00005753. 20-JAN-2003; 2003WO-FR000178. 06-MAY-2004 (first entry) Corvaia N, WPI; 2003-569653/53. WO2003059951-A2 Homo sapiens. 24-JUL-2003. Goetsch L, ADJ76913; RESULT 1 ADJ76913 

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these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate. Iung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastroinestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                            61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                          QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                     Gaps
                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human antibody 7C10 2 heavy chain variable region SEQ ID NO:79.
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                                                                                                                                                       Length 117;
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                                                                                                                                                      100.0%; Score 627; DB 7;
100.0%; Pred. No. 1.8e-48;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 13; SEQ ID NO 79; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                   ADZ67083 standard; protein; 117 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAX-2002; 2002FR-00005753.
20-JAN-2003; 2003MO-FR000178.
11-JUL-2003; 2003FR-00008538.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                       Best Local Similarity 100.
Matches 117; Conservative
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CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DUFLOS A. HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2005084906-A1.
                                                                                                                           Sequence 117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                 ADZ67083;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GOET/) (
(CORV/) (
(LEGE/) 1
                                                                                                                                                         Query Match
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(HAEU/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heavy
                                                                                                                                                                                                                                                                                                                                                       RESULT 2
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The invention relates to a novel isolated anti-insulin-like glowun lactor of the invention relates to a novel isolated anti-insulin-like glowun lactor capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor.

Comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induced intended of the insulin or receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF-dependent and/or HERZ/neu-dependent and/or EGF-dependent and/or HERZ/neu-dependent and/or IGFZ-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent cells, preferably IGF-dependent and/or EGF-dependent and/or EGF-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of psoriasis. (I) is useful in the preparation of a medicament intended for the specific targeting of a biologically active compound to intended for the specific targeting of a biologically active compound to intended for the specific targeting of a biologically active compound to intended for the specific targeting of the IGF-IR and/or EGFR receptor. (I) is useful for intended for the specific targeting of a biologically active compound to intended for the specific targeting of a biologically active compound to intended for the specific targeting the IGF-IR and/
novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of IGF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is useful for in vitro diagnosis of this coses and or GFR receptor overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF and an announce to ensemble the involves contacting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 627; DB 9;
100.0%; Pred. No. 1.8e-48;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ76915 standard; protein; 135 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 117 AA;
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69. .84 /note= "CDR2" '7. .124

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Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                               18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                           16-DEC-2003; 2003US-00735916.
                                                                                                                                                                                              2002FR-00000653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-321968/33.
                                                                                                                                                                                                                                                                                                     GOETSCH L.
CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADZ67084
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                                                                                        US2005084906-A1
                                                                                                                                                                                                                                                                                                                                                                                                 BECK A.
                                                                                                                                                                                              8-JAN-2002;
                                                                                                                           21-APR-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Goetsch L,
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(HAEU/)
                                                                                                                                                                                                                                                                                                       GOET/)
                                                                                                                                                                                                                                                                                                                                                                                                 BECK/)
                                                                                                                                                                                                                                                                                                                                           LEGE/)
                                                                                                                                                                                                                                                                                                                          CORV/)
   Region
                                     Region
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                                                                                                                                                                                                                                                                                                  The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with these receptors with their ligands. Especially they inhibit transformation of normal cells, so are useful against cancers of the prostate, unsy, breast, endomerrium and collon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lumor; endocrine disease; gynecology and objectics; breast tumor; endomerroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 135
                                                                                                                                                                                                             New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 627; DB 7; Length 135; Best Local Similarity 100.0%; Pred. No. 2e-48; Matches 117; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 81; 164pp; French.

    .18
    /note= "leader peptide"

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                                                                                                        (FABR ) FABRE MEDICAMENT SA PIERRE.
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                                                                                                                                          Corvaia N, Leger O;
                                                  18-JAN-2002; 2002FR-0000654.
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20-JAN-2003; 2003WO-FR000178
                                     18-JAN-2002; 2002FR-00000653
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                                                                                                                                                                                WPI; 2003-569653/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 135 AA;
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Ä; Beck

Duflos A, Haeuw J,

Leger O,

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The invention relates to a novel isolated anti-insulin-like growth factor

I receptor (IGF-IR) antibody (I) or its functional fragment, being
capable of binding to human IGF-IR and, if necessary, capable of
supplie of binding to human IGF-IR and, if necessary, capable of
capable of binding to human IGF-IR and, if necessary, capable of
specifically inhibiting tyrosine kinase activity of the receptor,
comprising a light or heavy chain having at least one complementary
determining region (GDR) consisting of one of two fully defined 16 amino
caids (Dazé7006 and ADZ67014). An antibody of the invention is useful in
the preparation of a medicament intended for the prevention or treatment
cof an illness connected with an overexpression and/or an abnormal
activation of the IGF-IR and/or EGFR, and/or connected with a
hyperactivation of the transduction pathway of the signal mediated by the
connected with Information of IGF-IR and/or EGFR, and/or of EGFR with EGFR, where
the administration of fhe medicament does not induce or only slightly
induces secondary effects connected with inhibition of the insulin
creeptor. The artibody is useful for preparation of a medicament intended
to inhibit the transformation of normal cells into cells with tumoral
character, preferably IGF-dependent, especially IGF and/or IGF2
dependent and/or EGF-dependent and/or HERZ/neu-dependent and/or IGF2-dependent and/or EGF-dependent
and/or the proliferation of umor cells, preferably IGF-dependent
and/or the proliferation of tumor cells, preferably IGF-dependent
and/or the proliferation of umor cells, preferably IGF-dependent
cells. (I) is useful in the preparation of a medicament intended for the specific targeting of a biologically scriv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.
Example 13; SEQ ID NO 81; 125pp; English.
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Gaps .; o

0; Indels

Mismatches

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115; Conservative

Matches

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or for epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit prowth and/or proliferation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                 78
                                                                                                                                                                                            79 KPSLKORVIISRDISKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVIVSS 135
                                                                                                                                                                    61 KPSLKDRVTISRDTSKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                 19 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLMWMIRQPPGKGLEWIGYISYDGTNNY
                                                                                            QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                          Gaps
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                 Score 627; DB 9; Length 135;
Pred. No. 2e-48;
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100.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; antipsoriatic; antibody;
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18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
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                                                        Matches 117; Conservative
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                                       Local Similarity
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                     Query Match
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99.4%; 98.3%;

Query Match Best Local Similarity

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Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lump tumor; endocrine disease; gynecology and obsterrics; breast tumor; endometroid carcinom; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal appraisation of the IGF-IR and/or EGFR, and/or connected with a hyperactivation of the transduction pathway of the signal mediated by the interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
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                                                                  KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                  KPSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                              QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                           Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.
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                                                                                                                                                                                        ADZ67079 standard; protein; 117
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07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                                                                                                                                                                                                                                     chain variable region.
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
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(HAEU/)
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insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; 1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60 61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117 KPSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFPDYWGQGTLVTVSS 117 0; Gaps Score 623; DB 9; Length 117; Pred. No. 4e-48; 0; Indels 2; Mismatches cytostatic; antipsoriatic; antibody; (FABR ) FABRE MEDICAMENT SA PIERRE. ADJ76911 standard; protein; 135 AA Leger 0; Anti-IGF-1R related protein #23. 18-JAN-2002; 2002FR-00000654. 07-MAY-2002; 2002FR-00005753. 99.4%; 20-JAN-2003; 2003WO-FR000178 18-JAN-2002; 2002FR-00000653 (first entry) Query Match
Best Local Similarity 98.3
Matches 115; Conservative Corvaia N, WPI; 2003-569653/53 Sequence 117 AA; WO2003059951-A2. Homo sapiens. 06-MAY-2004 24-JUL-2003 Goetsch L, ADJ76911; 19 유 \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$ ઠે ò g

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fragments, that bind to human insulan-like growth factor.1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulan-like growth factors.1 receptor (IGF-IR) and optionally: (ii) inhibit natural binding of insulan-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or compared as associated with overexpression and/or abnormal activity of IGF-IR. Ab and its fragments are used to prevent or IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with CGC these receptors with their ligands. Especially they inhibit cransformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protéin sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrites; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
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New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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                                                            Disclosure; SEQ ID NO 77; 164pp; French
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/note= "leader peptide"
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/note= "CDR2"
117. .124
/note= "CDR3"
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/note= "CDR1"
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Matches 115; Conservative
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insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;

cytostatic; antipsoriatic; antibody;

Anti-IGF-1R related protein #26.

06-MAY-2004 (first entry)

ADJ76917;

ADJ76917 standard; protein; 117 AA

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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyroshine kinase activity of the receptor, operation of being tyroshine kinase activity of the receptor, capable of specifically inhibiting tyroshine kinase activity of the receptor, determining region (CDR) consisting of one of two fully defined 16 amino acids (ADS67006 and ADS67014). An antibody of the invention is useful in a determining region (CDR) consisting of one of two fully defined 16 amino acids (ADS67006 and ADS67014). An antibody of the invention is useful in a lineas connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a phormal colf an illness connected with IGF-IR and/or EGFP with EGFP, where content of IGF or IGFP with IGF-IR and/or EGFP with EGFP, where interaction of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to Infunct and/or IGF2-dependent and/or IGF2-dependent and/or EGF-dependent of a medicament intended for prevention of the preparation of a medicament intended for prevention or for the treatment of cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for prevention or for the presention of a medicament intended for the specific targeting of a biologically active compound to reatment of psoriasis. (I) is useful in the preparation of a medicament intended for the specific targeting of a biologically and/or EGFR receptor: (I) is useful for in vitro diagnosis of illnesses induced by an expressing or an underexpression or an undere
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98.3%; Pred. No. 4.7e-48;
... Mismatches 0;
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                              07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
18-JAN-2002; 2002FR-00000654
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CORVAIA N.
LEGER O.
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                                                                                                                                                                                                                                                                                          DUFLOS A.
                                                                                                                                                                                                                                                                                                                            HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADZ67080
                                                                                                                                                                                                                                                                                                                                                                  BECK A.
                                 07-MAY-2002;
20-JAN-2003;
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                                                                                                                                                                                                                                                                                                                                                                  BECK/)
                                                                                                                                                                                 GOET/)
                                                                                                                                                                                                                                                    LEGE/)
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New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

(FABR ) FABRE MEDICAMENT SA PIERRE.

18-JAN-2002; 2002FR-00000654 07-MAY-2002; 2002FR-00005753

2002FR-00000653

18-JAN-2002;

20-JAN-2003; 2003WO-FR000178.

WO2003059951-A2. Homo sapiens.

24-JUL-2003

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Corvaia N,

Goetsch L,

WPI; 2003-569653/53.

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or reast diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epideral growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit prowth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPSLKDRVTISVDTSKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVXPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 615; DB 7;
Pred. No. 2.1e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
Disclosure; SEQ ID NO 83; 164pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 117 AA;
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RESULT 10

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19 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY 78

1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor.

Comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a cutivation of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2.
                                                                                                                                                                                                   neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent, especially IGF-dependent and/or IGF2-dependent and/or ERF2/neu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
                                                                                                                                                                                    Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
                                                                                                                                           Human antibody 7C10 3 heavy chain variable region SEQ ID NO:83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 13; SEQ ID NO 83; 125pp; English.
                       ADZ67087 standard; protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leger O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002FR-00000653
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11-JUL-2003; 2003FR-00008538
                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goetsch L, Corvaia N,
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CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DUFLOS A. HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                  US2005084906-A1.
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                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                       30-JUN-2005
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                                                              ADZ67087;
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(HAEU/)
(BECK/)
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(LEGE/)
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                                                                                                                                                                                                                                                    of IGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
breast cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) standy or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 KDSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYXCARYGRVFPDYMGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.1%; Score 615; DB 9; Length 11
98.3%; Pred. No. 2.1e-47;
ive 1; Mismatches 1; IndelB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; antipsoriatic; antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ76919 standard; protein; 135 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-IGF-1R related protein #27
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Matches 115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-569653/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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            these receptors with their ligands. Bepecially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and pass for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGP. IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
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hyperactivity of signal transduction pathways mediated by interaction of
                                                                                                                                                                                                                                                             61 KPSLKDRVTISRDTSKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                             KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 135
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                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Human antibody 7C10 3 heavy chain variable region SEQ ID NO:85.
                                                                                                                                                   Length 135;
                                                                                                                                                                             1; Indels
                                                                                                                                                   Score 615; DB 7;
Pred. No. 2.4e-47;
                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "leader peptide"
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                                                                                                                                                                                                                                                                                                                                                           ADZ67089 standard; protein; 135 AA
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/note= "CDR1"
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/note= "CDR2"
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/note= "CDR3"
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2002FR-00005753.
2003WO-FR000178.
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98.3%;
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                                                                                                                                                                              115; Conservative
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/note=
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Best Local Similarity
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
BECK A.
                                                                                                                        Sequence 135 AA;
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(CORV/)
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The invention fractional fragment, being capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of capable of the invention is useful in a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal connected with an overexpression and/or an abnormal connected with an intended for the signal mediated by the interaction of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induced administration of the medicament does not induce or only slightly induced to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF-dependent and/or EGF-dependent cells, preferably IGF-dependent and/or EGF-dependent cells, preferably IGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of psoriasis. (I) is useful in preparation or a medicament intended for the specific targeting of a biologically active compound to intended for the specific targeting of a biologically active compound to intended for the specific targeting of a biologically active compound to intended for the specific targeting of intended for the specific targeting of intended for the specific targeting of intended for the specific 
                                                                                                                                                                                                                                                                                    The invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present
                                                                                                 Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLMNWIRQPPGKGLEWIGYISYDGTNNY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYCARYGRVFFDYWGQGTLVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
     Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 615; DB 9; Length 135;
Pred. No. 2.4e-47;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence is used in the exemplification of the invention.
     Haeuw J,
Duflos A,
                                                                                                                                                                                                                                  Example 13; SEQ ID NO 85; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ76903 standard; protein; 117 AA
  Leger O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-IGF-1R related protein #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.1%;
98.3%;
                                                                                                                                                                             cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 98.3
Matches 115; Conservative
Corvaia N,
                                                  WPI; 2005-321968/33.
                                                                                                                                                                             useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 135 AA;
Goetsch L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ76903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ76903
  셤
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endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; heavy chain variable region.

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Fragments, that bind to human insulin-like growth factor-1 receptor (IGF) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) himbit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, one useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69.
                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to an isolated antibody (Ab), and its functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLMNWIRQFPGNKLEWMGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.3%; Score 541; DB 7; Length 117; 84.5%; Pred. No. 9e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 69; 164pp; French.
                                                                                                                                                                                                                                                                                                         (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADZ67073 standard; protein; 117 AA
                                                                                                                                                                                                                                                                                                                                              Leger 0;
                                                                                                                                                                                                                                                     18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                 20-JAN-2003; 2003WO-FR000178
                                                                                                                                                                                                                                    2002FR-00000653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                              Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-569653/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 117 AA;
                                                                                                                            WO2003059951-A2
                      or epidermal
                                                                                                                                                                                                                                    .8-JAN-2002;
   insulin-like
                                                                                           Homo sapiens.
                                                                                                                                                            24-JUL-2003
                                                                                                                                                                                                                                                                                                                                              Goetsch L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADZ67073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADZ67073
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activation of the transduction pathway of the signal mediated by the interaction of 1GF1 or 1GF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only alightly induces secondary effects connected with inhibition of the insulin creeptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral celestration. The arabicommation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2.

C dependent and/or EGF-dependent, especially IGF-dependent cells. (1) is useful for preparation of a medicament intended to inhibit the growth capecially IGF1-and/or IGF2-dependent and/or EGF-dependent of Intended for prevention or for the treatment of amedicament intended for the preparation of a medicament intended for the preparation of a medicament or cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (1) is useful in the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to services a services and a underexpression of the IGF-IR and/or EGFR receptor is suspected, which involves contacting the receptor is suspected, which involves contacting the EGFR receptor is suspected, which involves contacting the EGFR receptor is optionally labeled. The present correction of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a activation of the IGF-IR and/or EGFR, and/or connected with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 13; SEQ ID NO 69; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leger O,
                                                                                                                                                                                                                                                                                    18-JAN-2002; 2002FR-00000554.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                 16-DEC-2003; 2003US-00735916.
                                                                                                                                                                                                                                                               2002FR-00000653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-321968/33.
                                                                                                                                                                                                                                                                                                                                                                                              GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DUFLOS A. HAEUW J.
                                                                                                                              US2005084906-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BECK A.
                                                                                                                                                                                                                                                               .8-JAN-2002;
                                                                                       Mus musculus.
                                                                                                                                                                        21-APR-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soetsch L,
                                                                                                                                                                                                                                                                                                                                                                                                (GOET/)
(CORV/)
                                                                                                                                                                                                                                                                                                                                                                                                                                          (LEGE/)
(DUFL/)
(HAEU/)
(BECK/)
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Sequence 117 AA;

neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor;

Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells, so are useful against cancers of the prostate, lung, breate, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                           2 VOLOESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIROPPGKGLEWIGYISYDGTNNYK 61
                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                 2 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQPPGNKLEMMGYISYDGTNNYK
                                                                                                                                                         62 PSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                             62 PSLKDRISITRDISKNOFFLKLNSVINEDTATYYCARYGRVFFDYMGGGTTLIVSS 117
                                         Gaps
                                         ö
 Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein sequence used to generate the Ab of the invention
                                       8; Indels
y Match 86.3%; Score 541; DB 9; Local Similarity 84.5%; Pred. No. 9e-41; hes 98; Conservative 10; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 52; 164pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                             ADJ76886 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goetsch L, Corvaia N, Leger O;
                                                                                                                                                                                                                                                                                                                                                                                                          Anti-IGF-1R related protein #4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2002; 2002FR-0000653.
18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JAN-2003; 2003WO-FR000178
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003059951-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUL-2003
Query Match
Best Local S
                                       Matches
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Score 541; DB 7; Length 127; Pred. No. 9.8e-41;

86.3%;

Query Match Best Local Similarity

Search completed: January 10, 2006, 20:44:17 Job time : 80.7649 secs

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US-11-012-353-75
                     456.5
455.5
452.5
451.5
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 75, Appl Sequence 77, Appl Sequence 81, Appl Sequence 83, Appl Sequence 69, Appl Sequence 69, Appl Sequence 162, Appl Sequence 162, Appl Sequence 163, Appl Sequence 154, Appl Sequence 154, Appl Sequence 71, Appl Sequence 71, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 11, Appl Sequence 161, Appl Sequence 1619, Appl Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Appli
Sequence 1619, Ap
Sequence 17, Appl
Sequence 1994, Ap
Sequence 1329, Ap
Sequence 841, Appl
Sequence 112, App
                                                                                                                                                    ; Search time 5.96642 Seconds (without alignments) 166.558 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 110,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 77,
Sequence 79,
Sequence 81,
                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA_New:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-11-054-669-112
US-11-054-669-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                     61141 segs, 8493638 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                             protein search, using sw model
                                                                                                                                                           January 10, 2006, 20:55:23
                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 200000000
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628
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Sequence 75, Application US/11012353
; Sequence 75, Application US/2005049730A1
; Sequence 75, Application No. US2005049730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: HARUW, JEAN-FRANCOIS
; APPLICANT: NOWER: US/11/012,353
; CURRENT FILING DATE: 2003-12-16
; PRIOR FILING DATE: 2003-07-11
; PRIOR FILING DATE: 2003-07-11
; PRIOR FILING DATE: 2003-07-11
; PRIOR FILING DATE: 2002-01-18
                                                                          Sequence 155, Appl
Sequence 1659, Ap
Sequence 117, Appl
Sequence 127, Appl
Sequence 1745, Ap
Sequence 1745, Ap
Sequence 1597, Ap
Sequence 55, Appl
Sequence 55, Appl
Sequence 20, Appl
                                                                                                                                                                                                                                                                                                        Sequence 1510, Ap
Sequence 954, App
Sequence 1321, Ap
Sequence 1223, Ap
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100.0%; Pred. No. 8.7e-49;
iive 0; Mismatches 0;
US-11-054-515-1339

US-11-054-515-1578

US-11-054-515-1981

US-11-074-515-1981

US-11-074-515-1981

US-11-074-515-1659

US-11-054-515-167

US-11-054-515-167

US-11-054-515-167

US-11-054-515-167

US-11-054-515-1597

US-11-054-515-1597

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US-11-054-515-1597

US-11-054-515-1510

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Best Local Similarity 100.0
Matches 117; Conservative
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TYPE: PRT
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US-11-012-353-77

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WS-11-012-35
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Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: BUGKS, ALAIN
APPLICANT: BECR, OLIVIER
APPLICANT: BECR, OLIVIER
APPLICANT: BECR, OLIVIER
APPLICANT: ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: U0/735,916
PRIOR APPLICATION NUMBER: R003-07-11
PRIOR PLING DATE: 2003-07-11
PRIOR PLING DATE: 2003-07-11
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FCT/FR03/00178
PRIOR APPLICATION NUMBER: FCT/FR03/00178
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FCT/FR03/00178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-11-012-353-77
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TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REPERENCE: 017753-198

CURRENT PILING DATE: 2004-12-16

PRIOR PILING DATE: 2003-12-16

PRIOR PILING DATE: 2003-01-20

PRIOR PILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-01-20

PRIOR PILING DATE: 2003-01-20

PRIOR PILING DATE: 2003-01-20

PRIOR PILING DATE: 2003-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

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PRIOR PILING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.2%; Score 623; DB 7; Length 117; Best Local Similarity 98.3%; Pred. No. 2.4e-48; Matches 115; Conservative 2; Mismatches 0; Indels
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR PILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 81, Application US/11012353;
Publication No. US20050249730A1;
GENERAL INFORMATION:
APPLICANT: CORVAIA, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HAEUW, JEAN-FRANCOIS;
APPLICANT: LEGER, OLIVIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Ver. 3.3
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US-11-012-353-81
                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-11-012-353-79
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SEQ ID NO 81
LENGTH: 135
                                                                                                                                                                                                                                            LENGTH: 117
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TYPE: PRT; ORGANISM: Homo sapiens
US-11-012-353-85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-012-353-69
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     Sequence 83, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFRENCE: OllyTS3-198
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2003-12-16
PRIOR PELICATION NUMBER: FR 020653
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-01-20
PRIOR PLILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-05-07
PRIOR PRILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SSOFTWARE: PRIOR PRILING DATE: 2002-01-18
IERGTH: 117
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APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR APPLICATION NUMBER: 10/735,916
PRIOR PILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: RR 0308538
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR FILING DATE: 2003-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.3%; Score 611; DB 7;
Best Local Similarity 96.6%; Pred. No. 2.6e-47;
Matches 113; Conservative 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 85, Application US/11012353
Publication No. US20050249730A1
GRNERAL INFORMATION:
APPLICANT: GOSTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-11-012-353-83
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US-11-012-353-83
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Sequence 69, Application US/11012353

Sequence 69, Application US/11012353

Publication No. US200S0249730A1

GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
APPLICANT: GOETSCH, LILIANE
APPLICANT: GOETSCH, LILIANE
APPLICANT: LEGER, OLIVIER
APPLICANT: HEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR PELICATION NUMBER: 10/735,916
PRIOR PELICATION NUMBER: 10/735,916
PRIOR PELICATION NUMBER: PR 0308538
PRIOR PELICATION NUMBER: PR 0308538
PRIOR PELICATION NUMBER: PR 0200-07-11
PRIOR PELING DATE: 2002-07-07-11
PRIOR PELING DATE: 2002-07-07-11
PRIOR PELING DATE: 2002-07-07-11
PRIOR PELING DATE: 2002-01-08
PRIOR PELING DATE: 2002-01-18
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Pred. No. 1.2e-41;
8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 611; DB 7; Length 135; Pred. No. 3e-47; 3; Mismatches 1; Indels
PRIOR APPLICATION NUMBER: FK 0200053
PRIOR FILING DATE: 2002-05-07
PRIOR PLING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 85
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Best Local Similarity 86.2%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 96.6%;
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1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY 60
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84.6%; Pred. No. 2e-40;
ive 7; Mismatches 11; Indels
PRIOR FILING DATE: 2003-01-20
PRIOR PLING DATE: 2002-05-07
PRIOR PILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR APPLICATION NUMBER: FR 0200654
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTIN OF: 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 70, Application US/11012353; Publication No. US20050249730A1.
FUBLICATION NO. USZUBERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 91; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 99; Conserv
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                                                                                                                                                              Sequence 52, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
TITLE OF INVENTION: NOVEL ANTI-INSULIN/IGP-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGB-IR AND USES THEREOF
FILE REFRENCE: 01/1753-198
TITLE OF INVENTION: NOVEL ANTI-168
FILE REFRENCE: 01/1753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: FR 0308538
FRIOR APPLICATION NUMBER: FR 0308538
FRIOR FILING DATE: 2003-07-11
FRIOR FILING DATE: 2003-07-11
FRIOR FILING DATE: 2003-07-12
FRIOR FILING DATE: 2003-07-13
FRIOR FILING DATE: 2002-05-07
FRIOR PRILOR APPLICATION NUMBER: FR 020653
FRIOR FILING DATE: 2002-05-07
FRIOR PRILOR PRILOR DATE: 2002-01-08
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE:
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Sequence 162, Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GOETSCH, LILIANE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DUFLOS, ALAIN

APPLICANT: BECK, ALAIN

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-198

CURRENT APPLICATION NUMBER: 10/735,916

PRIOR FILING DATE: 2004-12-16

PRIOR FILING DATE: 2003-12-16

PRIOR PLILOGIATION NUMBER: PCT/FR03/00178

PRIOR APPLICATION NUMBER: PCT/FR03/00178
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          PSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
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Pred. No. 1.3e-41;
8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 86.9%;
Best Local Similarity 86.2%;
Matches 100; Conservative
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APPLICANT: CORVAIA, NATHALE
APPLICANT: CORVAIA, NATHALE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEW, LISANCOIS
APPLICANT: HAEW, LISANCOIS
APPLICANT: HAEW, CLIVIER
APPLICANT: HEGER, OLIVIER
APPLICANT: EGER, OLIVIER
APPLICANT: OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 020553
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-01-18
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61 NPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYMGQGTTLTVSS 117
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62 PSLKORISITRDTSKNQFFLKLASVTTEDTATYYCAREGYGYFPDYWGQGTTLTVSS 118
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Publication No. US2005025532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P3

CURRENT APPLICATION NUMBER: US/11/054,515

FRICE APPLICATION NUMBER: 00/543,296

PRIOR PILING DATE: 2004-02-11

PRIOR PLLING DATE: 2004-02-11

PRIOR PLLING DATE: 2004-06-18

PRIOR FILING DATE: 2004-06-18

PRIOR FILING DATE: 2004-1-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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US-11-054-515-1651
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61 KPSLKDRITISRDTSKNQPSLKLSSVTAADTAVYYCARY-----GRVF-FDYWGQGTLV 113
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PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR PELICATION NUMBER: 60/340,817
PRIOR PLILANG DATE: 2001-12-19
PRIOR PLILANG DATE: 2001-12-19
PRIOR PLILANG DATE: 2001-06-15
PRIOR PLILANG DATE: 2001-06-15
PRIOR PLILANG DATE: 2001-05-25
PRIOR PLILANG DATE: 2001-05-25
PRIOR PLILANG DATE: 2001-03-21
PRIOR PLILANG DATE: 2001-03-21
PRIOR PLILANG DATE: 2001-03-16
PRIOR PLILANG DATE: 2001-03-16
PRIOR PLILANG DATE: 2000-10-17
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US-11-054-515-1548

Sequence 1548, Application US/11054515

Publication No. US2005025532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P3

CURRENT APPLICATION NUMBER: US/11/054,515

FILOR APPLICATION NUMBER: 00/543,296

PRIOR PILING DATE: 2004-06-18

PRIOR PILING DATE: 2004-06-18

PRIOR PILING DATE: 2002-11-14

PRIOR PILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR PILING DATE: 2001-11-16

PRIOR PILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-31

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16
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NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1548
LENGTH: 250
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75.8%; Pred. No. 2.3e-35;
tive 7; Mismatches 16; Indels
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US-11-054-515-1651
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Best Local Similarity
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TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REPERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 259
TYPE: PRT
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                                                                                                                                                                                                                            PSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCAR----YGR-VFFDYWGQGTLVTVS 116
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                                                                                                        Gaps
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US-10-512-184-34
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                                                                                                      Indels
                                                                   76.0%; Score 477.5; DB 7; 75.8%; Pred. No. 2.3e-35;
                                                                                                      8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 34, Application US/10512184 Publication No. US20050244901A1 GENERAL INFORMATION:
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                                                                 Query Match
Best Local Similarity 75.81
Matches 94; Conservative
                ; ORGANISM: Homo sapiens
US-11-054-515-1548
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Best Local S
Matches 91
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: precursor OTHER INFORMATION: fusion protein comprising ACE - linker - OTHER INFORMATION: scFv PL2.
                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                       Length 371;
                                                                                                                                                                                                                                                                       ; Score 474.5; DB 6; Length
; Pred. No. 6.1e-35;
11; Mismatches 14; Indels
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CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                         75.6%;
                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.2*
Matches 91; Conservative
                     NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 71
LENGTH: 371
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US-10-512-184-71
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us-10-735-916a-75.rapbm

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Sequence 77, Application US/10735916A Publication No. US20050084906A1
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US-10-735-916A-77
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(c) 1993 - 2006 Compugen Ltd
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US-10-735-916A-75

Sequence 75, Application US/10735916A

Publication No. US2050084906A1

Publication No. US2050084906A1

APPLICANT: GOETSCH, Liliane

APPLICANT: GOETSCH, Liliane

APPLICANT: LEGER, Olivier

APPLICANT: DUFLOS, Alain

APPLICANT: BEER, Alain

APPLICANT: HAEUW, Jean-Francois

TITLE OF INVENTION: NOVEL ANTI-1GP-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-183

CURRENT FILING DATE: 2003-01-2-16

PRIOR PLING DATE: 2003-01-11

PRIOR PLING DATE: 2003-01-11

PRIOR PLING DATE: 2003-01-12

PRIOR FILING DATE: 2003-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-05-07

NUMBER OF SEQ ID NOS: 156

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US-10-292-088-98
US-10-292-088-70
US-10-292-088-70
US-10-310-719-35
US-10-984-960A-20
US-10-984-960A-20
US-10-805-177-114
US-10-802-306A-14
US-10-802-306A-14
US-10-988-360-10
US-10-988-360-10
US-10-309-762-138
US-10-309-762-138
US-10-309-762-138
US-10-309-762-138
US-10-309-762-138
US-10-309-762-138
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US-10-802-306A-9
US-10-802-306A-9
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         ORGANISM: Homo sapiens
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US-10-735-916A-79
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APPLICANT: CONVAIA, Nathalie
APPLICANT: CONVAIA, Nathalie
APPLICANT: DIGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: BONNEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: PR 03/08 538
PRIOR PILING DATE: 2003-01-1
PRIOR APPLICATION NUMBER: PR 02/00 654
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTIN VET. 2.1
LENGTH: 1177
TWOER: DRIT
                              APPLICANT: CORVAIA, Mathalie
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: HEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
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100.0%; Score 628; DB 5;
Best Local Similarity 100.0%; Pred. No. 5.1e-49;
Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                 Sequence 79, Application US/10735916A Publication No. US20050084906A1 GENERAL INFORMATION:
APPLICANT: GOETSCH, Liliane APPLICANT: CORVAIA, Nathalie
                      APPLICANT: GOETSCH, Liliane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
  GENERAL INFORMATION:
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1 OVOLOESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
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                                                                                                                                               1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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                                                                           Gaps
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APPLICANT: GOSTSCH, Liliane
APPLICANT: GOSTSCH, Liliane
APPLICANT: GOSTSCH, Liliane
APPLICANT: GOSTACH, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REPERENCE: 017753-183
CURRENT APPLICATION NUMBER: RS 03/08 538
FRIOR FILING DATE: 2003-01-16
FRIOR APPLICATION NUMBER: PCT/FR 03/00 178
FRIOR FILING DATE: 2003-01-20
FRIOR FILING DATE: 2002-01-18
FRIOR PILING DATE: 2002-01-18
FRIOR APPLICATION NUMBER: FR 02/00 653
FRIOR APPLICATION NUMBER: FR 02/00 654
FRIOR APPLICATION NUMBER: FR 02/00 53
FRIOR APPLICATION NUMBER: FR 02/00 54
FRIOR APPLICATION NUMBER: FR 02/00 55
FRIOR APPLICATION NUMBER: FR 02/00 55
FRIOR APPLICATION NUMBER: FR 02/05 753
FRIOR APPLICATION NUMBER: FR 02/05 753
FRIOR APPLICATION NUMBER: FR 02/05 753
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Publication No. US20050084906A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, Liliane
APPLICANT: LEGER, Olivier
APPLICANT: BUFLOS, Alain
APPLICANT: HECK, Alain
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   Length 117;
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                                                                       0; Indels
Score 623; DB 5;
Pred. No. 1.2e-48;
                                                                   2; Mismatches
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99.2%;
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SOFTWARE: PatentIn Ver. 2.1
                                                                       Matches 115; Conservative
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US-10-735-916A-81
Query Match
Best Local Similarity
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19 QVQLQESGPGLVXPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 78
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US-10-735-916A-69
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APPLICANT: CORVER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: BUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGP-IR ANTIBODIES AND USES THEREOF
TITLE REPERENCE: 01773-183
CURRENT APPLICATION: NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
PRIOR PILING DATE: 2003-01-11
PRIOR PILING DATE: 2003-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: PRIOZ-01-18
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97.3%; Score 611; DB 5;
Best Local Similarity 96.6%; Pred. No. 1.7e-47;
Matches 113; Conservative 3; Mismatches 1
                           CURRENT PERIOR NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: RC 03/08 538
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-01-18
SOFTWARE: PARENT FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PARENT NOS: 1156
SEQ ID NO 83
LENGTH: 117
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-735-916A-83
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US-10-735-916A-85
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61 KPSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                      2 VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK
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Sequence 69, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION

APPLICANT: GOETSCH, Liliane

APPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: DUFLOS, Alain

APPLICANT: BEEK, Alain

APPLICANT: WINGER: US/10/735,916A

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE PREFERENCE: 017753-183

CURRENT APPLICATION NUMBER: FR 03/08 538

PRIOR APPLICATION NUMBER: FR 02/00 654

PRIOR FILING DATE: 2003-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18
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Sequence 52, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:
APPLICANT: GOETSCH, Liliane
APPLICANT: CORVAIA, Nathalie
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A

CURRENT FILIAGO DATE: 2003-12-16
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86.9%; Score 546; DB 5; Length 117;
Best Local Similarity 86.2%; Pred. No. 1.1e-41;
Matches 100; Conservative 8; Mismatches 8; Indels
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PRIOR APPLICATION NUMBER: FR 03/08 538
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
PRIOR PILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 02/00 653
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APPLICANT: Powers, Daniel
APPLICANT: Powers, Daniel
APPLICANT: Powers, David
TITLE OF INVENTION: Antibodies Against Cancer Antigen TMEFF2 and Uses Thereof
FILE REPERENCE: 05882.0138.NPUS00
CURRENT APPLICATION NUMBER: US/10/383,447
PRIOR PAPLICATION NUMBER: US 60/362,837
PRIOR PILING DATE: 2002-03-08
PRIOR FILING DATE: 2002-03-08
PRIOR FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                     Length 127;
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                                                                                                                                                                                                                                                                                                                     Query Match 86.9%; Score 546; DB 5; Best Local Similarity 86.2%; Pred. No. 1.2e-41; Matches 100; Conservative 8; Mismatches 8
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 52
LENGTH: 127
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Publication No. US20040096392A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bhaskar, Vinay
APPLICANT: de la Calle, Agustin
APPLICANT: Law, Debbie
APPLICANT: Caras, Ingrid
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Afar, Daniel
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US-10-383-447-24
; Sequence 24, Application US/10383447
                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-52
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LENGTH: 120
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APPLICANT: Caras, Ingrid
APPLICANT: Caras, Ingrid
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Afar, Daniel
APPLICANT: Powers, Daviel
APPLICANT: Powers, Daviel
APPLICANT: Afar, Daniel
APPLIC
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APPLICANT: de la Calle, Agustin
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Murray, Richard
APPLICANT: Repersor Savid
TITLE OF INVENTION: Antibodies Against Cancer Antigen TMEFF2 and Uses Thereof
FILE REFERENCE: 05802-03-03
FILE REPERSOR SAVID NUMBER: US/10/383,447
CURRENT FILING DATE: 2002-03-07
PRIOR PELLING DATE: 2002-03-08
PRIOR FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 60/463,812
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APPLICANT: Bhaskar, Vinay
APPLICANT: de la Calle, Agustin; APPLICANT: Law, Debbie
                                                                            APPLICANT: Bhaskar, Vinay
APPLICANT: de la Calle, Agustin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
SEQ ID NO 28
LENGTH: 120
US20040096392A1
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Best Local Similarity 81.5%
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us-10-735-916a-75.rapbm

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Query Match
Best Local Similarity
Matches 98; Conserv
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                                                              2 VOLOBSGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK 61
                                                                                      2 VQLQBSGPGLVKPSETLSLTCAVSGYSITSGYYWSWIRQPPGKKLEWMGFISYDGSNKYN 61
                                                                                                                                                                      62 PSLKNRITISRDISKNOFSLKLSSVTAADTATYYCARGLRRGDYSMDYWGQGTLVTVSS 120
                                                                                                                                              62 PSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCA---RYGRVFFDYWGQGTLVTVSS 117
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                        3; Gaps
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Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Grads, Vaan
APPLICANT: Holtz, Ian
APPLICANT: Holtz, Ian
APPLICANT: Holtz, Ian
APPLICANT: Holtz, Ian
APPLICANT: Gallo, Michael
TITLE OF INVENTION: (A.I.) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT APPLICATION NUMBER: 60/337275
PRIOR APPLICATION NUMBER: 60/337275
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
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                        13; Indels
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  83.2%; Pred. No. 2.8e-38;
tive 4; Mismatches 13
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Publication No. US20030211100A1
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
COURANT APPLICATION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/10/292,088
CURRENT FILING DATE: 2003-03-14
PRIOR FILING DATE: 2003-03-14
PRIOR FILING DATE: 2001-11-09
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 109
LENGTH: 116
                      99; Conservative
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US-10-309-762-143
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US-10-292-088-109
    Best Local Similarity
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US-10-292-088-109
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US-10-309-762-143
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APPLICANT: DELEGATION OF THE APPLICANT: DELEGATION OF THE APPLICANT: Tee, Kam Fai APPLICANT: Tee, Kam Fai APPLICANT: Useffers, Michael APPLICANT: Mesti, Mehdi APPLICANT: Mesti, Mehdi APPLICANT: Mestes, Peter APPLICANT: Mestes, Peter APPLICANT: Khramtsov, Mikolia APPLICANT: Khramtsov, Mikolia APPLICANT: Khramtsov, Mikolia APPLICANT: Khramtsov, Mikolia APPLICANT: Mestes ABKCUR: 0004 NUMBER: Us/10/805,177
CURRENT APPLICATION NUMBER: Us/10/805,177
PRIOR PILING DATE: 2004-03-19
PRIOR FILING DATE: 2003-03-19
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                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
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 DB 4; Length 118;
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                                      Indels
79.7%; Score 500.5; DB 4;
llarity 82.4%; Pred. No. 1.5e-37;
Conservative 6; Mismatches 12;
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Pred. No. 1.8e-37;
6; Mismatches 13
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 121
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81.7%;
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US-10-805-177-56
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Best Local Similarity
Matches 98; Conserv
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7
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Best Local Similarity 80.5%; Pred. No. 1.9e-37;
Matches 99; Conservative 5; Mismatches 12; Indels 7; Gaps
; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 25; LEWGTH: 122; TYPE: PT TYPE: PT TYPE: PT ORGANISM: Homo sapiens US-10-309-762-25
                                                                                                                                                                                                                                                                                             Search completed: January 10, 2006, 21:35:32 Job time : 64.1754 secs
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Sequence 3, Ay
Sequence 2, Ay
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                            Sequence 7, Sequence 9, Sequence 5, Sequence 5, Sequence 5, Sequence 5,
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81.7%; Pred. No. 4.8e-42;
ive 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                            Sequence 39, Application US/09025769B

Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Fack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Go, Liming
APPLICANT: Go, Liming
APPLICANT: Pluckthun, Andreas
ITILE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
US-09-343-698-6
US-08-35-95-6
US-08-30-927-453-7
US-09-273-453-7
US-08-36-13A-9
US-08-450-578-5
US-09-017-628-5
US-09-017-628-5
US-09-017-628-5
US-09-017-628-5
US-09-467-903-5
US-08-450-363-5
US-08-55-5
US-08-55-5
US-08-55-5
US-08-55-5
US-08-77-128-18
US-08-77-128-18
US-08-77-128-18
US-08-77-128-18
                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.7
Matches 98; Conservative
   TOPOLOGY: linear
MOLECULE TYPE: protein
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Sequence 39,
Sequence 39,
Sequence 65,
Sequence 2, A
Sequence 13,
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Sequence 39,
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*
(cgn2_6/ptodata/1/iaa/f_COMB.pep:*
(cgn2_6/ptodata/1/iaa/f_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-09-490-153-65

US-09-490-153-65

US-09-490-153-65

US-09-490-324-65

US-09-490-324-65

US-09-490-324-65

US-09-049-672h-4

US-09-049-672h-4

US-08-137-117D-69

US-08-137-117-69

US-08-137-117-69
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US-09-138-091A-77
US-10-330-613A-1
US-10-330-613A-17
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US-10-330-613A-5
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                                                                                                                                                                                                                                                              572060 segs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
                                                                                                   January 10, 2006, 20:34:27
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628
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seq length: 200000000
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Match Length
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                       QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY 59
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: Eloppy disk

COMPUTER: Eloppy disk

COMPUTER: Eloppy disk

COMPUTER: Datual PC-DOS/MS-DOS

SOFTWARE: PACHILI Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr, 98G.

REGISTRATION NUMBER: MORPHO/5

TELEPHONE: (212)596-9000

INFORMATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: mino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STRET: 1251 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                               APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                          Sequence 65, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 81.7
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-025-769B-65
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US-09-490-070A-39; Sequence 39, Application US/09490070A; Patent No. 6696248

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61 KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 65, Application US/09490070A
; Sequence 65, Application US/09490070A
; Patent No. 669624B
; Patent Normanian Sequence Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 119;
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                                                                                                                           Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INPORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTATION NUMBER: 31,298
REPERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 912-2000
TELEPAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 496; DB 2;
Pred. No. 4.8e-42;
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-490-070A-65
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RESULT 6
US-09-490-153-65
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Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James P. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
                                                                                   COUNTRY: USA
ZIP: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPUTED:
COMPUTER: PC COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
79.0%; Score 496; DB 2; Length 119;
Best Local Similarity 81.7%; Pred. No. 4.8e-42;
Matches 98; Conservative 6; Mismatches 12; Indels
White & McAuliffe
6 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY ARENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-490-153-39; Sequence 39, Application US/09490153; Patent No. 6706484; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acida
TYPE: amino acid
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Pack, Peter
Ilag, Vic
                                             CITY: Washington STATE: D.C.
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61 KPSLKDRITISRDISKNOFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 79.0%; Score 496; DB 2; Length 119; Best Local Similarity 81.7%; Pred. No. 4.8e-42; Matches 98; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moroney, Simon
Plueckthut, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & STREET: 1251 Avenue of the Americas
            PRIOR PELLICATION DATA:

PRIOR APPLICATION DATA:

PILLING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILLING DATE: 18-NG-1995

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 27,794

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-900

TELEPHONE: (212)596-900

INFORMATION FOR SEQ. ID NO: 39:

SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acida
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-153-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 65, Application US/09490153;
Patent No. 6706484;
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Ilag, Vic
Ge, Liming
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FILING DATE: 24-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10021
COMPUTER READABLE FORM:
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STATE: New York
COUNTRY: USA
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CITY: New York
                                     Query Match
Best Local Similarity
Matches 98; Conserv
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  US-09-490-324-39
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                                                                                                                                                                                                                                                                                                                                                                                                                             29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            Length 119;
                                                                                                                                                                                                                                                                                  12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCES: 373
                                                                                                                                                                                                                                          Score 496; DB 2;
Pred. No. 4.8e-42;
6; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/490,324
PILING DATE: 24-3an-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-R040-1995
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REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFRAT: (212)596-9000
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                TELEPHONE: (212)596-9000
TELEFAX: (212)596-9000
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 39, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
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Best Local Similarity 81.7%;
Matches 98; Conservative
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ZIP: 10021
COMPUTER READABLE FORM:
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61 KPSLKDRITISRDISKNQFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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                                                                                                                           1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
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                                                                                             1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 496; DB 2; Length 119;
Pred. No. 4.8e-42;
6; Mismatches 12; Indels
  Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
Score 496; DB 2;
Pred. No. 4.8e-42;
6; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-199
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-324-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                        Sequence 65, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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79.0%;
81.7%;
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Best Local Similarity 81.7%;
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                 Conservative
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61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGD-GFDYWGQGTLVTVSS 117

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ZUCHANTER READABLE FORM:

MEDIUM TYPE: Diskette COMPUTER: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Cerrone, Michael C
REGISTATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                     Sequence 4, Application US/09049672A Patent No. 6135941
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 77.2
Matches 98; Conservative
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CLONE: 1513264
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-049-672A-4
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1 QVQLQESGPGLVKPSETLSLTCTVSGYSI-TGGYLWNWIRQPPGKGLEWMGYISYDGTNN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGLEWIGSIYHSGSTYY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.9%; Score 483; DB 2; Length 117; Best Local Similarity 81.4%; Pred. No. 9.3e-41; Matches 96; Conservative 6; Mismatches 14; Indels
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Patent No. 6924360

GENERAL INFORMATION:

APPLICANT: Gudas, Jean

TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN

FILE REFERENCE: ABGENIX.022A

CURRENT APPLICATION NUMBER: 05/24

CURRENT PLING DATE: 2002-12-26

PRIOR PLING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

NUMBER OF SEQ 1D NOS: 90

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                             GENERAL INPORMATION:
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Williams, Andrew J
APPLICANT: Tempest, Philip R
APPLICANT: Main, Sarah H
APPLICANT: Daramola, Helen
TITLE OF INVENTION: Improvements relating to antibodies
FILE REFERENCE: AHB/CPS/75333
CURRENT ALING DATE: 2002-10-23
CURRENT ELLING DATE: 1998-07-02
                                                                                                                                                                                                                           Sequence 2, Application US/09720493
Patent No. 6827925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-330-613A-13
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LENGTH: 117
TYPE: PRT
                                                                                                                                                          RESULT 9
US-09-720-493-2
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60 YKPSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCAR------YGRVFFDYWGQG 110
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APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Corley, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
CORRESPONDENCE ADDRESS:
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APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: RESHARED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                            ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-08-137-117D-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCAR--YGRVFFDYWGQGTLVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.8%; Score 482; DB 1; Length 123; Best Local Similarity 75.6%; Pred. No. 1.2e-40; Matches 90; Conservative 11; Mismatches 16; Indels
         Sequence 64, Application US/08137117D

Patent No. 5795965

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki

APPLICANT: BENDIG, Mary

APPLICANT: JONES, Steven

APPLICANT: AALDANHA, Jose

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

ITTLE OF INVENTION: INTERLEUKIN-6 RECEPTOR

NUMBER OF SEQUENCES:

ADDRESSE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
COUNTRY: USA
ZIPE: 20007-2109
COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IEM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRICA APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRICA APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRICA APPLICATION NUMBER: JS-25476
FILING DATE: 25-APR-1991
APPLICATION NUMBER: JS-35476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HAROLD C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5309
                                                                                                                                                                                                                                                     STREET: SOON K Street, N.W., Suite 500 CITY: Washington STATE: D.C. CUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 904136
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 123 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-137-117D-64
       US-08-137-117D-64
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US-08-436-717-64
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5 QVQLQESGPGLVRPSQTLSLTCTVSGYSITSDHAMSWVRQPPGRGLEWIGYISYSGITTY 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.8%; Score 482; DB 1; Length 123; 75.6%; Pred. No. 1.2e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Indels
                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/436,717 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Mismatches
                                                                                                                                                                                                                              CLASSIPCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
FRIGH GAPE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: JP 5-487-1091
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HAICOLG C.
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 69, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, JOSE
                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
ZIP: ZO007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
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Sequence 64, Application US/08436717 Patent No. 5817790 GENERAL INFORMATION: APPLICANT: TSUCHIYA, Masayuki

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Washington
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TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN NUMBER OF SEQUENCES: 158
CORRESPONDENCES: 158
CORRESPONDENCES: 158
CORRESPONDENCES: 158
COUNTY. USA
ZIF: Washington Kireet, N.W., Suite 500
CITY: Washington Kireet, N.W., Suite 500
COUNTY: USA
ZIP: 20007-5109
COMPUTER: DEADLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 20-DEC-1993
CLASSIPICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-ARR-1992
RRIOR APPLICATION NUMBER: WP 4-32084
FILING DATE: 25-ARR-1992
RRIOR APPLICATION NUMBER: JP 9-32084
FILING DATE: JP-REB-1992
RRIOR APPLICATION NUMBER: JP 3-95476
FILING DATE: Z5-ARR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGISTRATION NUMBER: Z5-Z58
RREPERRENCE/DOCKET NUMBER: S3466/126/AAOK
TELECOMMUNICATION INFORMATION:
NAME: WEGISTRATION INFORMATION:
TELEPHONE: (20026725300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: BANDG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 69, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 138 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-436-717-69
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STATE: D.C.
COUNTRY: U.S.
COUNTRY: U.S.
COUNTRY: U.S.
COMPUTER: Floppy disk
COMPUTER: Elegopy disk
COMPUTER: Elego
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RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                 ADJ76909
                                                                                   ; Search time 80.7649 Seconds (without alignments) 636.505 Million cell updates/sec
                                                                                                                                          US-10-735-916A-75
628
1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117
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version 5.1.6
- 2006 Compugen Ltd.
                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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                                                                                       January 10, 2006, 20:07:41;
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Listing first 45 summaries
                                                          protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adj76909 Anti-IGF-	Adz67079 Human ant	Adj76911 Anti-IGF-	-	Adj76913 Anti-IGF-	6	Adj76915 Anti-IGF-	S	Adj76917 Anti-IGF-	_	Adj76919 Anti-IGF-		Adj76903 Anti-IGF-		Adj76886 Anti-IGF-	Adz67056 Murine im	Adc27457 Humanised	Adc27455 Humanised	Adc27459 Humanised	Aay15126 Anti-muri	Adp03973 Murine-ex	Ads16559 Human ant	Adp03885 Murine-ex	Adp03889 Murine-ex
SUMMARIES	ΩΙ	. `	ADZ67079	ADJ76911	ADZ67081	ADJ76913	ADZ67083	ADJ76915	ADZ67085	ADJ76917	ADZ67087	ADJ76919	ADZ67089	ADJ76903	ADZ67073	ADJ76886	ADZ67056	ADC27457	ADC27455	ADC27459	AAY15126	ADP03973	ADS16559	ADP03885	ADP03889
	DB	7	σ	7	σ	7	σ	7	σ	7	δ	7	σ	7	σ	7	δ	7	7	7	m	7	æ	7	7
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di	Query	100.0	100.0	100.0	100.0	99.2	99.2	99.5	99.2	97.3	97.3	97.3	97.3	86.9	86.9	86.9	86.9	84.6	81.4	81.0	80.5	80.1	80.0	79.5	79.5
	Score	. 9	628	628	628	623	623	623	623	611	611	611	611	546	546	546	546	531.5	511.5	508.5	505.5	503	502.5	499.5	499.5
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Adp03958 Murine-ex	Adp03957 Murine-ex	Abb07171 ebvHigM M	Adi26658 Human ant	Adp03887 Murine-ex	Adp03884 Murine-ex	_	Abj18676 Antibody	Ade28455 Human ant	Ade28479 Human ant	Ady74798 Human 1gG	Aec20804 Low+ mode	Aec20877 Low + mod	Aay44615 Human ant	Ade28491 Human ant	Ade28471 Human ant	Aao30915 dI-NHS76	Aao30913 dI-NHS76	Aea21456 Human ant	Adx98267 Human ant	Ads16505 Human ant	
ADP03958	ADP03957	ABB07171	ADI26658	ADP03887	ADP03884	AAW27554	ABJ18676	ADE28455	ADE28479	ADY74798	AEC20804	AEC20877	AAY44615	ADE28491	ADE28471	AA030915	AA030913	AEA21456	ADX98267	ADS16505	
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120	116	121	121	122	122	119	119	121	466	119	118	467	117	121	466	280	580	122	139	121	
79.4	79.1	79.1	79.1	79.1	79.1	79.0	79.0	79.0	79.0	78.7	78.6	78.6	78.5	78.5	78.5	78.5	78.5	78.3	78.3	78.1	
498.5	496.5	496.5	496.5	496.5	496.5	496	496	496	496	494	493.5	493.5	493	493	493	493	493	491.5	491.5	490.5	
25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

### ALIGNMENTS

insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR. New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers. (FABR ) FABRE MEDICAMENT SA PIERRE. ADJ76909 standard; protein; 117 AA Anti-IGF-1R related protein #22. Leger O; 18-JAN-2002; 2002FR-0000653. 18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-00005753. 20-JAN-2003; 2003WO-FR000178. 06-MAY-2004 (first entry) Goetsch L, Corvaia N, WPI; 2003-569653/53. WO2003059951-A2 Homo sapiens. 24-JUL-2003. ADJ76909; 

Disclosure; SEQ ID NO 75; 164pp; French.

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or rear diseases associated with overexpression and/or abnormal activity of IGF-IR and/or receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of

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these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                        KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                          KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
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                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.
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                                                                                                                                                      Length 117;
                                                                                          protein sequence used to generate the Ab of the invention
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                                                                                                                                                                                    ö
                                                                                                                                                    Score 628; DB 7;
Pred. No. 3.2e-49;
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                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 13; SEQ ID NO 75; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                   ADZ67079 standard; protein; 117 AA
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                                                                                                                                                    100.0%;
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20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                  Matches 117; Conservative
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CORVAIA N.
LEGER O.
                                                                                                                                                                   Local Similarity
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                                                                                                                          Sequence 117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JAN-2002;
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                                                                                                                                                      Query Match
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(LEGE/)
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The invention relates to a novel isolated anti-insulin-like grown ractor of receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of pecifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary comprising a light or heavy chain to the light of the distriction of the invention of useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal critication of the IGF-IR and/or EGFR, and/or connected with a more consected with an overexpression of the signal mediated by the interaction of the IGF-IR and/or EGFR, and/or connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent cells, preferably IGF-dependent and/or IGF2-dependent cells, preferably IGF-dependent and/or IGF2-dependent cells, is preferably IGF-dependent and/or IGF2-dependent and/or IGF2-dependent cells, it is useful in the preparation of a medicament intended for prevention or for the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, contended for the preparation of a medicament intended for the prevention or for the preparation of a medicament intended of a biologically and/or IGF2-dependent cells in vitro diagnosis of illnesses induced by an efficient of sequence is useful in vibro diagnosis of illnesse
a novel isolated anti-insulin-like growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGFGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 628; DB 9;
100.0%; Pred. No. 3.2e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic, antipsoriatic, antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003059951-A2.
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Sequence 135 AA;
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
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                                                                                                                                                                                                      New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein sequence used to generate the Ab of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 628; DB 7;
100.0%; Pred. No. 3.8e-49;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "leader peptide"
49. .54
                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 77; 164pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                   (FABR ) FABRE MEDICAMENT SA PIERRE.
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20-JAN-2003; 2003WO-FR000178.
                                18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
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Matches 117; Conservative
                                                                                                                                                                        WPI; 2003-569653/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 135 AA;
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                                                                                                                                     Goetsch L,
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The invention relates to a novel isolated anti-insulinities being capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyroshine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a cativation of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induced interaction of the medicament does not induce or only slightly induced induced secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGFI-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or IGF2-dependent and/or IGF2-dependent and/or EGF-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or EGF-dependent cells, preferably IGF-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the preparation of a medicament intended for the specific targeting of a biologically active compound to intended for the specific targeting of a biologically active compound to intended for the specific targeting of a biologically active compound to intended for invite intended for the specific targeting of a biologically active compound to intended for the specific targeting of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel isolated anti-insulin-like growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beck A;
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                                  "CDR2"
                                                                                                                   /note= "CDR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2002; 2002FR-00000554.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
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69. .84
/note= "
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CORVAIA N.
LEGER O.
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HAEUW J.
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Gaps

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Indels

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Mismatches

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Conservative

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Matches

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGP-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or fight overexpression and/or abnormal activity of IGF-IR and/or signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit around transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating pseriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insulin-like growth factor-1 receptor; IGP-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                              KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                   KPSLKDRITISRDISKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGGGTLVIVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                               QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                      QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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Score 628; DB 9;
Pred. No. 3.8e-49;
                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; antipsoriatic; antibody;
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                                                                                                                                                                                                                                                                                                     ADJ76913 standard; protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-IGF-1R related protein #24.
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100.0%;
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18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
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                  Local Similarity 100.
Les 117; Conservative
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Length 117;

Score 623; DB 7; Pred. No. 9.2e-49;

99.2%;

Query Match Best Local Similarity

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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGP-IR) antibody (I) or its functional fragment, being capable of binding to human IGP-IR and, if necessary, capable of specifically inhibiting tronine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal hyperactivation of the IGP-IR and/or connected with a hyperactivation of the transduction pathway of the signal mediated by the interaction of IGF1 or IGF2 with IGP-IR and/or of EGF with EGFR, where
                                                                                                                                                                                                                                                                                                             neoplasm; prostate tumor; andrology; genttourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; synecology and obsterrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                           QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                             1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                   Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
                                                                                                                                                                                                                                                                       Human antibody 7C10 2 heavy chain variable region SEQ ID NO:79.
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2002FR-00005753.
2003WO-FR000178.
2003FR-00008538.
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
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07-MAY-2002;
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the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin creeptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral chearacter, preferably IGF-dependent, especially IGF1 and/or IGF2.

CC dependent and/or EGF-dependent and/or EREX/neu-dependent cells. (I) is useful for preparation of tumor cells, preferably IGF-dependent, and/or the proliferation of tumor cells, preferably IGF-dependent, cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breat cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriais. (I) is useful in preparation of a medicament contended for the special in preparation of a medicament contended for the prevention or for the compound to cells expressing or overexpressing of a biologically active compound to cells expressing or overexpressing of the IGF-IR and/or EGFR receptor of starting from a biological sample with (I), which is optionally labeled. The present of seminare is useful if the invention of the invention. sequence is used in the exemplification of the invention Sequence 117 AA; 

ö 9 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLBWMGYISYDGTNNY 60 KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 0; Gaps 99.2%; Score 623; DB 9; Length 117; 98.3%; Pred. No. 9.2e-49; ive 2; Mismatches 0; Indels Best Local Similarity 98.3 Matches 115; Conservative Н Н 61 61 Query Match 셤 g ઠ 8

ADJ76915

ADJ76915 standard; protein; 135 AA

ADJ76915;

(first entry) 06-MAY-2004 Anti-IGF-1R related protein #25.

insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; cytostatic; antipsoriatic; antibody;

Homo sapiens

WO2003059951-A2.

24-JUL-2003

8-JAN-2002; 2002FR-00000653

20-JAN-2003; 2003WO-FR000178

18-JAN-2002; 2002FR-00000654. 07-MAY-2002; 2002FR-00005753.

(FABR ) FABRE MEDICAMENT SA PIERRE.

Leger O; Goetsch L, Corvaia N,

WPI; 2003-569653/53 

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or creat diseases associated with overexpression and/or abnormal activity of IGF-IR. Ab and its fragments are used to prevent or IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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                                                                                Disclosure; SEQ ID NO 81; 164pp; French
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Matches 115; Conservative
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ADZ67085 standard; protein; 135 AA. ADZ67085 RESULT

ADZ67085;

(first entry) 30-JUN-2005 Human antibody 7C10 2 heavy chain variable region SEQ ID NO:81.

Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.

Homo sapiens.

l. .18 /note= "leader peptide" Location/Qualifiers .54 .= "CDR1" 69. .84 /note= "CDR2" 117. .124 /note= "CDR3" /note= Peptide Region Region Region 

US2005084906-A1.

21-APR-2005.

16-DEC-2003; 2003US-00735916.

18-JAN-2002; 2002FR-00000653

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The invention relates to a novel isolated anti-insulin-like growth factor capable of capable of binding to human IGP-IR and, if necessary, capable of specifically inhibiting to human IGP-IR and, if necessary, capable of specifically inhibiting tynoshine kinase activity of the receptor, capable of specifically inhibiting tynoshine kinase activity of the receptor, determining a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in a cids (ADZ67006 and ADZ67014). An antibody of the invention is useful in a liness connected with an overexpression and/or a bnormal of an illness connected with IGP-IR and/or EGFR, and/or connected with an abnormal coll of the IGP-IR and/or EGFR, and/or connected with an edited with interaction of the transduction pathway of the signal amediated by the interaction of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulant receptor. The antibody is useful for preparation of a medicament intended contact preferably IGP-dependent, especially IGP-dependent cells into calls with tumoral character, preferably IGP-dependent, especially IGP-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent cells, in the preparation of a medicament intended for prevention or too the treatment of cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of percentage or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful in preparation of a medicament intended for the specific targeting of the IGF-IR and/or EGFR receptor. (I) is useful in vitro daysonses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor is useful for in vitro daysonses induced which the abnormal presence is used in the exemplification of the present of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
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aa.3%; Pred. No. 1.1e-48;
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2002FR-00005753.
2003WO-FR000178.
                                                                         11-JUL-2003; 2003FR-00008538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                Goetsch L, Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2005-321968/33.
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                                                                                                                                               GOETSCH L.
CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADZ67084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                      BECK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                      (BECK/)
                                                                                                                                                                                  (CORV/)
(LEGE/)
                                                                                                                                                                                                                                                            (DUFL/)
(HAEU/)
                                                                                                                                               GOET/)
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-12 and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or creat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or prolater, lung, breast, endometrium and colon, also osteosarcoma, and slos of treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                          inaulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKFSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 611; DB 7;
Pred. No. 1.1e-47;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 83; 164pp; French.
                                                                                                                                                             cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FABR ) FABRE MEDICAMENT SA PIERRE.
                ADJ76917 standard; protein; 117 AA.
                                                                                                                          Anti-IGF-1R related protein #26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                18-JAN-2002; 2002FR-0000654.
                                                                                                                                                                                                                                                                                                                                                                             20-JAN-2003; 2003WO-FR000178
                                                                                                                                                                                                                                                                                                                                                                                                                   18-JAN-2002; 2002FR-00000653
                                                                                       06-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-569653/53.
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                                                                                                                                                                                                                                                                                                         WO2003059951-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 117 AA;
                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                          24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goetsch L,
                                                    ADJ76917;
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ADJ76917
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RESULT 10

KPSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117 

61

1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY

ö 9 78

Gaps ; 0

Indels

Matches 115; Conservative

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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino caids (ADZ67004). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal convertivation of the IGF-IR and/or EGFR, and/or connected with a chyperactivation of the transduction pathway of the signal mediated by the interaction of IGFI or IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly connected with inhibition of the insulin receptor. The antibody is useful fors preparation of a medicament intended connected with inhibit the growth character, preferably IGF-dependent, especially IGF-dependent and/or EGF-dependent and/or HERZ/neu-dependent and/or IGF-adependent and/or IGF-dependent and/or IGF-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                 neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                            growth factor 1 receptor; antibody; tumor; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
                                                                                                                                                                                                                                                                                                     Human antibody 7C10 3 heavy chain variable region SEQ ID NO:83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duflos A,
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                                         ADZ67087 standard; protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leger O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002FR-0000654.
2002FR-00005753.
2003WO-FR000178.
2003FR-00008538.
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                                                                                                                                                                                                                       (first entry)
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CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DUFLOS A. HAEUW J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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11-JUL-2003;
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                                                                                                                                ADZ67087;
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(HAEU/)
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ADZ67087
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preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the prevention of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor. (I) starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with
                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insulin-like growth factor 1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                               QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                        Length 117;
                                                                                                                                                                                sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                     97.3%; Score 611; DB 9;
96.6%; Pred. No. 1.1e-47;
ive 3; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; antipsoriatic; antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-IGF-1R related protein #27.
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                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                       Sequence 117 AA;
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                                                                                                                                                                                                                                                                                        Matches 113;
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                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                              Best Local
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       888888888888888
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                      these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
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hyperactivity of signal transduction pathways mediated by interaction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KPSLKDRITISRDTSKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
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                                                                                                                                                                                                                                                                                                 Length 135;
                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                    97.3%; Score 611; DB 7; 96.6%; Pred. No. 1.3e-47;
                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADZ67089 standard; protein; 135 AA
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`^= "CDR1"
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. "CDR2"
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2002FR-00005753.
2003WO-FR000178.
2003FR-00008538.
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/note= "CDR3"
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/note=
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                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
                                                                                                                                                                                                                                                 Sequence 135 AA;
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20-JAN-2003;
11-JUL-2003;
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(HAEU/)
(BECK/)
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The invention relates to a novel isolated and infinite, being grown capable of binding to human IGF-TR and, if necessary, capable of capable of binding to human IGF-TR and, if necessary, capable of expable of binding to human IGF-TR and, if necessary, capable of appetitionally inhibiting tyrosine kinase activity of the erceptor, comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary capable of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF IR and/or EGFR, and/or connected with a cativation of the IGF IR and/or EGFR, and/or connected with capable of interaction of the medicament does not induce or only slightly induces accordary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended contains the transformation of normal cells into cells with tumoral character, preferably IGF-dependent and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent cells, preferably IGF-dependent and/or the proliferation of a medicament intended for preparation of a medicament intended for preparation of a medicament intended for prevention or for the reatment of psecially IGF-dependent cancer, coton ancer (i) is useful in the preparation of a medicament intended for the prevention or for the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, the cancer is chosen from prostate cancer, osteosarcoma, lung cancer (contended for the prevention or for the preparation of a medicament intended for the prevention of a medicament intended for the prevention of a medicament intended for the prevention of a underexpression or the cancer is chosen from prostate cancer, os
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                                                                                                                                                                                                                                                      The invention relates to a novel isolated anti-insulin-like growth factor
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                                                                                   Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 KPSLKORVIISVDISKNQPSLKLSSVTAADTAVYYCARYGRVFPDYWGQGTLVIVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
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  Beck
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Pred. No. 1.3e-47;
3; Mismatches 1; Indels
Haeuw J,
Duflos A,
                                                                                                                                                                                                        Example 13; SEQ ID NO 85; 125pp; English.
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Leger O,
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Best Local Similarity 96.6
Matches 113; Conservative
Corvaia N,
                                             WPI; 2005-321968/33.
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Goetsch L,
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insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 PSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
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86.2%; Pred. No. 8.9e-42;
ive 8; Mismatches 8;
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
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                                                                                                                                       WO2003059951-A2.
                                                                                                  Homo sapiens
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, operation of binding tyrosine kinase activity of the receptor, determining region (CDR) consisting of one of two fully defined 16 amino cide (ADZ67014). An antibody of the invention is useful in catefactament of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a moverexpression and/or an abnormal contraction of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where interaction of the ransduction pathway of the signal mediated by the interaction of IGFO or IGF2-IR and/or EGFR, and/or of EGF with EGFR, where contracter, preferraby is useful for preparation of a medicament intended contracter, preferraby IGF-dependent, especially IGF1 and/or IGF2-dependent and/or HERZ/neu-dependent cells into calls with tumoral capendian and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent cells, in the preparation of a medicament intended for prevention or tor the treatment of cancer, where the cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of sorgials. (I) is useful in the preparation of a medicament intended for prevention or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psorials. (I) is useful in the preparation of a medicament intended for the prevention or colon cancer. (I) is useful in the specially active compound to the specific targeting of a biologically active compound to intended for the specific targeting of a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor IR and/or EGFR receptor (I) which involves co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; heavy chain variable region.
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                                                                                                                                                                                                                                                           18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003MO-FR000178.
11-JUL-2003; 2003FR-00008538.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for treating
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CORVAIA N.
LEGER O.
DUFLOS A.
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                                                                                     Mus musculus
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                                                                                                                                                                                                                                                                                                                                                            (GOET/)
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Sequence 117 AA

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (1) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (1i) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or the overexpression and/or abnormal activity of IGF-IR and/or pidernal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and prostate, lung, breast, and are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insulin-like growth factor-I receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
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                                                                                                                                                                                         VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLMNWIRQPPGNKLEMMGYISYDGTNNYK
                                                                                                                                                       VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                   PSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                         PSLKDRISITRDISKNOFFLKLNSVINEDTATYYCARYGRVFFDYWGOGTTLIVSS 117
                                                                               Gaps
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       Length 117;
                                                                           8; Indels
86.9%; Score 546; DB 9;
86.2%; Pred. No. 8.9e-42;
iive 8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 52; 164pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ76886 standard; protein; 127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leger O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-IGF-1R related protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2002; 2002FR-00000653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JAN-2003; 2003WO-FR000178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                           Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goetsch L, Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-569653/53
                                         Best Local Similarity
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       Query Match
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Length 127;

Score 546; DB 7; Pred. No. 9.7e-42;

86.9%; 86.2%;

Query Match Best Local Similarity

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                                   71
                          12 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK
                                                     2 VOLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK
Gaps
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Search completed: January 10, 2006, 20:44:17 Job time : 81.7649 secs

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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

January 10, 2006, 20:28:02; Search time 14.1157 Seconds (without alignments) 797.508 Million cell updates/sec Run on:

US-10-735-916A-75 628 1 QVQLQESGPGLVKPSETLSL.......RYGRVFFDYWGQGTLVTVSS 117 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: 283416

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	variable reg	heavy	heavy chain	heavy	heavy chain V	heavy	heavy	heavy	heavy	heavy	heavy	heavy chain	heavy	heavy	heavy	heavy chain	heavy	heavy	heavy	heavy cha	pothetical	Ig heavy chain pre							
Ω	137782	S31690	830530	813519	S24443	831511	837200	807637	S30534	S31586	S38718	S44114	831512	S78052	878055	128195	S44113	AVMS35	E25114	A49045	S78051	S31676	809711	S47010	C53285	S20780	S30752	A24770	B24672
th DB	:		123 2				121 2											137 1			135 2					118 2	149 2		
Leng	1																												
t C	80.4	78.0		75.5			•	73.3	•	73.2	73.0	73.0	72.9	72.9	72.5	72.5	72.1	72.1	72.0	72.0	71.8	71.4	71.3	71.1	7.07	70.6	70.5	70.4	70.3
Scor	505	490	477	474	465.5	464	463	460.5	459.5	459.5	458.5	458.5	458	457.5		455	453	453	452	452	451	448.5	448	446.5	444	443.5	443	442	441.5
ω. ·	-	73	m	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19		21	22	23		25	26	27	28	29

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### ALIGNMENTS

RESULT 1
Iq variable region (VDJ) (clone T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C; Accession: 137782; S25476
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A, Title: Somatic diversification in the heavy chain variable region genes expressed by i
A; Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: 137782
A;Status: preliminary
A; Molecule type: mRNA
A;Residues: 1-140 <res></res>
A; Cross-references: UNIPARC: UP10000176E83; EMBL: X67906; NID: 93582; PIDN: CAA48104.1; PIL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
p. 46-120 /Domain immingalobilin homology /IMMs

	ω,	09	78	114
	8; Gaps	DGTNNY	SGSTNY	OGTLVT
	8;	YISY	XIX	DYYG
; Length 140;	9; Indels	WIROPPGKGLEWMG	HILLIIIII WIRQPPGKGLEWIG	ARYGRVFF
80.4%; Score 505; DB 2; Length 140;	BEST LOCAL SIMILATILY 81.3%; FIEU. NO. 3.20-39; Matches 100; Conservative 6; Mismatches 9; Indels	LTCTVSGYSITGGYLWN	20 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY 78	61 KPSLKDRITISRDISKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVT 114
80.48;	vative	GLVKPSETLS	GLVKPSETLS	ISRDISKNOF
1	Conse	LOESGI	LOESG	LKORI
tch	al Simi 100;	1 000	20 QVQ	61 KPS
Query Match	Best Loc Matches	ò	οp	λŏ

138 VSS 140 115 VSS 117 쉽 8 셤

RESULT 2 S31690

Johany chain V region - human (fragment)

C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: S31680
R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R; Chaisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R; Chestion: Machanisms that generate human immunoglobulin diversity operate from the A; Recreace number: S31585
A; Accession: S31690
A; Accession: S31690
A; Accession: S31690
A; Residues: 1-130 <CUI.
A; Molecule type: mRNA
A; Residues: 1-130 <CUI.
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin

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A; Molecule type: mRNA
A; Residues: 1-118 <-JON>
A; Cross-references: UNIPARC:UPI0000115FE9; EMBL:X61650; NID:g37720; PIDN:CAA43831.1; PII
A; Cross-references: UNIPARC:UPI0000115FE9; EMBL:X61650; NID:g37720; PIDN:CAA43831.1; PII
R; Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A; Title: By-passing immunization. Human antibodies from V-gene libraries displayed on pl
A; Reference number: $19663; MUID:92085276; PMID:1748994
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A, Status: mRNA
A, Molecule type: mRNA
A, Residues: 1-155 < CHIA>
A, Cross-references: UNIPARC: UPI00001160FF; EMBL: X69866; NID: 933094; PIDN: CAA49500.1; PII
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin homology < IMM>
P, 47-129/Domain: immunoglobulin homology < IMM>
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31511
S;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
S;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
S;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
S;Demitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA A;Reference number: S31509
A;Accession: S31511
                                                                                                                                                                                                                                                                                                                           60 YKPSLKDRITISRDISKNOPSLKLSSVIAADTAVYYCAR----YGRVFFDYWGQGTLVTV 115
                                                                                                                                                                                                                                                                                                                                                                            87 YNPSLKSRVTISVDTISKNQFSLKLSSVTAADTAVYYCARPLLWFGEL-FDYWGQGTLVTV 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C, Louis 12-Jan-1993 #Sequence_revision 22-Jan-1993 #text_change 20-Jun-2000 C, Accession: $24443; $19667  
R; Jones, P.T. submitted to the EMBL Data Library, October 1991 A; Reference number: $24442  
A; Accession: $24443  
A; Molecular  
A; Mol
                                                                                                                                                                   1 QVQLQESGPGLVKPSETLSLTCTVSGYSI-TGGYLWNWIRQPPGKGLEWMGYISYDGTNN
                                                                                                                                                                                                                27 QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLBWIGSIYYSGSTY
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                                                                                          Gaps
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            Length 147;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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                                                                                              14;
        Score 474; DB 2;
Pred. No. 2.3e-36;
7; Mismatches 14
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Best Local Similarity 77.3%; Pred. No. 1.1e-35;
Matches 92; Conservative 8; Mismatches 16
75.5%;
                                                 Best Local Similarity 77.9
Matches 95; Conservative
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A;Residues: 1-55,57-118 <MAR>
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Ig heavy chain - human
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Nucleic Acids Res. 19, 673, 1991
A; Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked A; Recession: S13519
A; Reference number: S13519; MUID:91187691; PMID:2011536
A; Accession: S13519
A; Residues: 1-147 *MOR>
A; Residues: 1-147 *MOR>
A; Residues: 1-147 *MOR>
A; Cross-references: UNIPARC:UPI0000115EBS; EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PIC C; Seywords: heterotetramer; immunoglobulin homology c; Keywords: heterotetramer; immunoglobulin homology cIMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGSSVLLWFGELLYYFDYWGQGT 124
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                                                                                                                                                                                                                                                                                                                           64
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Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                              6 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWSRQPPGKGLEWIGYIYYSGSTNY
                                                                                                                                                                                                                                                 1 OVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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R; Mariette, X.
submitted to the EMBL Data Library, October 1992
A; Reference number: S30520
A; Accession: S30530
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-123 < MAR>
A; Cross-references: UNIPARC: UPI0000176C83; EMBL: Z18316
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.0%; Score 477; DB 2; Length 123; Best Local Similarity 75.8%; Pred. No. 1e-36; Matches 94; Conservative 9; Mismatches 13; Indels
                                                                                              Length 130;
                                                                                     'Match 78.0%; Score 490; DB 2; Length 13 Local Similarity 77.0%; Pred. No. 7e-38; tes 97; Conservative 8; Mismatches 11; Indels
            F;20-102/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region - human
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                                                                                              Query Match
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Accession: S31586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UP1000011646E; EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PIC;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 YKPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCA------RYGRVFFDYW 107
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                 20 VQLQESGPGLVKPSQSLSLTCSVTDFSITSGYYWHWIRQFFGNKLEWMGYISYDGSNGYN 79
VOLOESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK 61
                                                                                            PSLKDRITISRDISKNOPSLKLSSVTAADTAVYYCAR-YGRVFFDYWGQGTLVTVSS 117
                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGSYYWSWIRQPAGKGLEWIGRIYTSGSTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVQLQESGPGLVKPSETLSLTCTVSGYSI - TGGYLWNWIRQPPGKGLEWMGYISYDGTNN
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer: immunoglobulin
F;Is-99/Domain: immunoglobulin homology <IMM>
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76.9%; Pred. No. 4.6e-35;
iive 7; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 th 73.2%; Score 459.5; DB 2 Similarity 71.5%; Pred. No. 4.3e-35, 93; Conservative 7; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, October 1992 A;Reference number: $30520 A;Accession: $30534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V region - human (fragment) C; Species: Homo ganiens (---)
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Best Local Similarity 76.37
Local 93; Conservative
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A;Molecule type: mRNA
A;Residues: 1-139 <CUI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <MAR>
                                                                                                                                                                                                                                                                                                                                    C; Accession: S30534
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                                                                                              62
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C; Species: Mus musculus (house mouse)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C; Accession: 337200
R; Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A; Description: Production and cloning of TMV-specific monoclonal antibodies.
A; Reference number: 337200
A; Accession: 337200
A; Accession: 337200
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-121 *eFIS>
A; Residues: 1-121 *eFIS>
A; Residues: 1-121 *eFIS>
A; Residues: UNIPARC:UPI00001161AC; EMBL:X74587; NID:9402639; PID:9402640
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; 15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                              91
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                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLMNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                                                           33 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYTGSATY
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       Length 155;
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                                                    14; Indels
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  Score 464; DB 2;
Pred. No. 2e-35;
9; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 73.7%; Score 463; DB 2; Best Local Similarity 73.3%; Pred. No. 1.9e-35; Matches 88; Conservative 11; Mismatches 17
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C;Superfamily: immunoglobulin V region; immunog
C;Kywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology <IMM>
    Query Match 73.9%;
Best Local Similarity 75.0%;
Matches 93; Conservative
                                                                                                                                                                                                                                                                                         114 TVSS 117
                                                                                                                                                                                                                                                                                                                                         152 TVSS 155
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Janeary Lorent Tunnan (Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Date: 13-Jan-1995 #sequence_revision: Date: 13.15.2
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc
A;Reference number: 83150
A;Recession: 831512
A;Return : preliminary
A;Molecule type: mRNA
A;Residues: 1-155 cffla
A;Cross-references: UNIPARC:UP100001160F9; EMBL:X69860; NID:g33082; PIDN:CNA49494.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
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A; Residues: 1-140 cHAR.
A; Cross-references: UNIPARC:UPI0000115E89; EMBL:X54441; NID:937815; PIDN:CAA38308.1; PII
A; Cross-references: UNIPARC:UPI0000115E89; EMBL:X54441; NID:937815; PIDN:CAA38308.1; PII
R; Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
Int. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and P
patient.
A; Reference number: S23716; MUID:92031262; PMID:1718404
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C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78052; S23717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 QVQLQQWGAGLLKPSETLSLTCAVYGGSFS-GYYWSWIRQPPGKGLEWIGEINHSGSTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYTGSATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OVOLOBSGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 155;
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A;Residues: 15-111 cHAW>
A;Cross-references: UNIPARC:UP10000116417; EMBL:X54441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.9%; Score 457.5; DB 2; Length 71.7%; Pred. No. 7.1e-35; ive 9; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 458; DB 2;
Pred. No. 7.1e-35;
8; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Harindranath, N. submitted to the EMBL Data Library, August 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 72.9%;
1 Similarity 73.4%;
91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: S78051
A;Accession: S78052
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nes 91; Conserv
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Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVSS 155
                                                                                                     Ig heavy chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S23717
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44114
C;Accession: Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable A;Bescription: Idiotypic vaccination against human B-cell lymphoma: rescue of variable A;Accession: S44105
A;Accession: S44114
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-129 cHAM>
A;Cross-references: UNIPARC:UPI0000116639; EMBL:Z31579; NID:g472968; PIDN:CAA83451.1; P
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                               Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 338718
R;Cimanis, A.Y.
Submitted to the EMBL Data Library, November 1993
A;Reference number: S38713
A;Recession: S38718
A;Status: preliminary
A;Status: preliminary
A;Gross-references: UNIPRAC:UP10000117542; EMBL:X76018; NID:g416102; PIDN:CAA53605.1; E;Superfemily: immunoglobulin V region; immunoglobulin homology
C;Superfemily: immunoglobulin homology <IMM>
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61 KPSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVF-----FDYWGQGTLV 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 PSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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Pred. No. 4.7e-35;
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75.0%;
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Best Local Similarity
Matches 89; Conserv
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Apacession: S78051
A; Accession: S78055
A; Residues: 1-145
A; Riberance (The genes encoding the V(H) and V(L) regions of low- and h patient.
A; Residues: S23716; MUD: 92031262; PMID: 178404
A; Recession: S23720
A; Molecule type: mRNA
A; Residues: 18-115
A; Residues: 18-115
A; Residues: 18-115
A; Residues: UNIPARC: UPI00001769D2; EMBL: X54445
A; Ccossion: S2370
A; Mote: the authors translated the codon GCA for residue 67 as Arg
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: immunoglobulin V region; immunoglobulin homology
C; Reywords: immunoglobulin H #status predicted <S1G>
F; 1-17/Domain: signal sequence (fragment) #status predicted <MAT>
F; 127/Domain: immunoglobulin homology <IMM>
A; 2-115/Domain: immunoglobulin homology <IMM>
A; Accession: A; Acce
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61 KPSLKDRITISRDISKNOFSLKLSSVTAADTAVYYCAR-----YGR-VFFDYWGQ 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain precursor V-D-J region (clone mAB 67VH) - human (fragment) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) S; Species: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999 C; Accession: S78055; S23720 R; Harindranath, N. Submitted to the EMBL Data Library, August 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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Query Match
77.2%; Score 485; DB 2; Length 119;
Best Local Similarity 78.3%; Pred. No. 3.6e-42;
Matches 94; Conservative 9; Mismatches 13; Indels
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                                                                               January 10, 2006, 20:26:41; Search time 78.8731 Seconds (without alignments) 1046.577 Million cell updates/sec
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1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117
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Q6gmx1
Q61bq5
Q5u413
Q6gmx7
P01822
Q53vq5
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Q7z379
Q96ey0
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Q569b8
Q86ex2
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                                                                                                         2166443 seqs, 705528306 residues
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06GWX HUWAN

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06UA13_MUUSE

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17379_HUWAN

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HV60_MOUSE
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QWWUX4_HUMAN
Q9BUIO_HUMAN
Q9GMX5_HUMAN
Q96AA6_HUMAN
Q912D7_HUMAN
Q81ZD7_HUMAN
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Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
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1: uniprot_sprot:*
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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The smaller human VH gene families display remarkably little

"The smaller human VH gene families display remarkably little

"The smaller human VH gene families display remarkably little

"The smaller human VH gene families display remarkably little

"EMBD J. 8:3741-3748 [1989].

"EMBL; AR035041; AAD56277.1; -; mRNA.

R PIR; PR0876; PR0876.

R PIR; S12416; S12416.

R PRSP; PO1820; 1G71.

"EMR; Q9UL73; 1-119.

"EMR; Q9UL73; 1-119.

"EMRSP: PO1820; IPR001596; Ig_V.

"EMART; SM00406; IGv; 1.

"MON MED.

"MON MED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLECTIDE SEQUENCE.
MEDLINE-98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Mt X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
Q53vq9 1
Q53vr6 1
Q5nyh3 1
Q53vr2 1
Q53vr2 Q5m83 1
Q53vg0 1
Q51vg0 1
Q9u175 P01823 1
Q7c3x7 P18532 m
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"Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.";
J. Exp. Med. 174:1639-1652(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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Clin. Immunol. Immunopathol. 87:184-192(1998)
                          OS3VR6_MOUSE
OS1VR3 HUWAN
OS10L9 RAT
OS3VR2_MOUSE
OS3VR2_MOUSE
HV47_MOUSE
HV47_MOUSE
HV47_MOUSE
HV2F_HUWAN
O9UL75_HUWAN
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Q7Z3Y6 HUMAN
HV61 MÕUSE
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ID Q9UL73 HUMAN PRELIMINARY;
AC Q9UL73 (777 MPEMBLEE). 1
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NUCLEOTIDE SEQUENCE.
PubMed=1660528;
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PubMed=2511001;
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NCBI_TaxID=9606;
     408
403.55
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20 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-GYYWSWIRQPAGKGLEWIGRIYTSGSTNY 78
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XI STAUSBORG R. L., Felngold E. A., Grouse L.H., Derge J.G.,

XI STAUSBORG R. L., Felngold E. A., Grouse L.H., Derge J.G.,

XI STAUSBORG R. L., Felngold E. A., Grouse L.H., Derge J.G.,

XI Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Diatchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

A Baba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robat S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XI Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XI Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rabesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Shutterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Roberzation and initial analysis of more than 15,000 full-length human
                                                                       59
 9
                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                 QVQLQESGPGLVKPSETLSLTCTVSGGSIC-SYYWSWIRQPPGKGLEWIGXIYYSGSTNY
  QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                           61 KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCAR---YGRVFFDYWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 465;
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073766; AAH73766.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 465 Aa; 51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 76.4%; Score 479.5; DB 2; Local Similarity 80.3%; Pred. No. 5.9e-41; Nes 94; Conservative 7; Mismatches 15;
                                                                                                                                                            465 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
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InterPro; IPR001359; IG.
InterPro; IPR00110; Ig-like.
InterPro; IPR001369; Ig Gl.
InterPro; IPR001369; Ig MHC.
InterPro; IPR001369; Ig W.
Pfam; PF07654; Cl-set; 3.
SMART; SM00407; IGC1; 3.
SWART; SM00407; IGC1; 3.
                                                                                                                                            6 HUMAN
QGGMX6 HUMAN PRELIMINARY;
QGGMX6;
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1 QVQLQESGPGLVXPSETLSLTCTVSGYSITGGYLMNWIRQPPGKGLEHMGYISYDGTNNY

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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Strausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Atlausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
Atlausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
Atlausner R.D., Marchaina K., Parmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marchaina K., Parmer A.A., Rubin G.M., Hong L.,
Atapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., William P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Kettemen M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M.,
Ruterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerthon and initial analysis of more than 15,000 full-length human
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61 KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                     79 NPSLKSRVITMSVDITSKNQPSLKLSSVTAADTAVYYCARGRFTYPDYWGQCTLVITVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VOLGESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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CTRAIN-MIX FVB/N;
CTRSUE_Ammmary tumor. WAP-TGF alpha model. 7 months old;
TISSUE_Ammmary tumor. WAP-TGF alpha model. 7 months old;
NIH MGC Project;
LSUDmitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
REMBL; BC002091; AAH02091.1; -; mRNA.
RHSSP; P01820; 1G7-1; -; mRNA.
RICEPTO; IPR007110; IG-1ike.
RICEPTO; IPR00710; IG-1ike.
RICEPTO; IPR003597; IG-C1.
RICEPTO; IPR003597; IG-C1.
RICEPTO; IPR003596; IG-V.
REMART; SM00406; IGV; 1.
RSMART; SM00406; IGV; 1.
RROSITE; PS50835; IG LIKE; 4.
RROSITE; PS50299; IG-MC; UNKNOWN_2.
RIMMINOGLOBULIN GOMEAIN.
W IMMUNOGLOBULIN GOMEAIN.
SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
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                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                     479 AA
                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 75.9%
hes 88; Conservative
                                                                                                                                                                                                                                                  Q99M22_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     LOC238447 protein.
Name=LOC238447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Mix FVB/N;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 460.5; DB 2
Pred. No. 1.4e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.3%;
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                                                                                                                                                                                                                                                                                                                                                      VH gene product (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87; Conservative
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Q5U413;
                                                                                                                                                                                                                                    QGLBQS_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                      TLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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NUCLEOTIDE SEQUENCE.
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                                                                                                               140 TMVTVSS
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MOUSE
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Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Antendenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toohlyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKennan R.J., McKernan K.J., Malek J.A., Gunzarene P.H.,
Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schain J.E., Jones S.J.M., Marra M.A.,
Scherzation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 YKPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYG----RVF----FDYWGQG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQPPGKGLEWIGXIYYSGSTY 79
                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                  80 PSLKARISITRDTSKNQFFLKLNSVTTEDTATYYCASRGYSWFPNWGQGTLVTVSA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL: BC073773; AAH73773.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 476 AA; 52206 MW; 622AABASC62DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human)
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InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003590; IG_MHC.
InterPro; IPR003590; IG_MHC.
InterPro; IPR003590; IG_MHC.
InterPro; IPR003590; IG_WHC.
InterPro; IPR003590; IG_V.
Pfam; PF07654; C1-8et; 3.
SWART; SW00409; IG; 2.
SWART; SW00406; IGv; 1.
PROSITE; PS00290; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                 QGGMX1_HUMAN PRELIMINARY;
QGGMX1;
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Matches
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VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 VQLQESGPGLVKPSQSLSLTCSVTDFSITSGYYWHWIRQFPGNKLBWMGYISYDGSNGYN
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus.
                                                                                                                                                                       MUCLECTIDE SEQUENCE.
MEDLINE=90067954; PubMed=2587273;
Urakov D.N., Deev S.M., Polyanovsky O.L.;
Urakov D.N., Deev S.M., Polyanovsky O.L.;
"The structure of the expressible VH gene from a hybridoma producing monoclonal antibodies against porcine transferrin.";
Nucleic Acids Res. 17:9481-9481(1989).
EMBL; X16749, CAA34714.1; -; Genomic_DNA.
HSSP; P18532; 1KCV.
SMR; Q6L8Q5; 20-136.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.V.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 VQLQESGPDLVKPSQSLSLTCTVTGYSITSGYGWHWIRQFPGNKLEWMGYISYSGSNNYN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 PSLKSRISITRDISKNOPFLOLNSVITEDIATYYCARYEGNYDYAMDYMGGGTSVIVSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 PSLKDRITISRDISKNOFSLKLSSVIAADIAVYYCARYGRVF---FDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VOLOESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.3%; Score 460.5; DB 2; Length 483; 73.9%; Pred. No. 5.7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                  STRAIN=FVB/N; TISSUE=Colon;
NIH MGC Project;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMAKI; SMUSIN, 15.1, 15.1, 18.3, 4.
PROSITE; PS00290; IG_MHC; UNKNOWN 2.
CERTIENCE 483 AA; 52714 MW; 7C272DAS01A4A0D1 CRC64;
                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo eaglens (Human).
                                                                                                                                                                                                                                                                                                                        EMBL, BC08512; AHH8512.1; -; mRNA.
Ensembl, BKNWUSG000054328; Mus musculus.
GO, GO.003823; F: snarigen binding; IEA.
InterPro; IPR00310; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003566; Ig.
Fram; PF07654; Cl-set; Z.
SMART; SM00409; IG; 3.
SWART; SM00400; IGV; 1.
Altschul S.F., Zeeberg B., Buetow K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGGMX7_HUMAN PRELIMINARY;
QGGMX7;
                                                                                                                                                                                                                             cDNA sequences.
                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                               and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Ab Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S. M. Worly D.W., Sodergran E.J., Lu X., Gibbs R.A., Av Villalon D.K., Muzny D.M., Sodergran E.J., Lu X., Gibbs R.A., Av Mithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Rodriguez A.C., Grimwood J., Schnutz J., Myers R.M., Rodriguez A.S., Grimwood J., Schnutz J., Myers R.M., Grenerth J.B., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 KPSLKDRITISRDISKNOFSLKLSSVTAADTAVYYCARYGRVF---FDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQTAGKGLEWIGYISHSGSTTY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89238351; PubMed=2497341; DOI=10.1016/0161-5890(89)90133-8; Rinfret A., Horne C., Dorrington K.J., Klein M.; "Cloning, sequencing and expression of the rearranged MOPC 315 VH gene segment.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
IG DARY-2005 (Rel. 47, Last annotation update)
IG Deavy chain V region MOPC 315 precursor.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butheleostomi;
Mammalia; Butheria; Euarchontcollires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWR; OGGWX7; 277455.

GO; GO:0016021; C:integral to membrane; IEA.

InterPro; IFR003599; Ig.
InterPro; IFR003599; Ig.
InterPro; IFR003599; Ig.
InterPro; IFR003599; Ig.
InterPro; IFR003596; Ig.
InterPro; IFR003596; Ig.
InterPro; IFR003596; Ig. V.
Ffam; PR07654; CI-set; Z.
SWART; SW00409; IG; 4.
SWART; SW00409; IG; 4.
SWART; SW00406; IGv; 1.
FROSITE; PS00296; IG_WIC; UNKNOWN_Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073765; AAH73765.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.0%; Score 458.5; DB 2
75.8%; Pred. No. 9.1e-39;
ive 11; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
PROTEIN SEQUENCE OF 1-31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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P01822;
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62 PSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCA----RYGRVFF---DYWGQGT 111
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harindranath N., Goldfarb I.S., Ikematsu H., Burastero S.E., Wilder R.L., Notkins A.L., Casali P.; "Complete sequence of the genes encoding the VH and VL regions of low-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VOLOESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWWNIRQFPGNKLEWMGYISYDGSHNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
"The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Clires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οĘ
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"Clonal proliferation of Igw secreting B cell in the synovium
Behcet's patient with arthritis.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03378; CAA27095.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 AA; 13931 MW; 502E51A5213F056E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VH4 heavy chain variable region precursor (Fragment)
                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 452; DB 2;
Pred. No. 9.4e-39;
                                                                                                                                                                           119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Mismatches
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01-WAY-1999 (TrEMBLrel. 10, Last seq
01-WAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                        PRT;
                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                         13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
VH-D-JH region (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.0%;
                                                                                                                                                                                                                               (TrEMBLrel. 31, (TrEMBLrel. 31, (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 72.09
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     095973 HUMAN PRELIMINARY;
                                                                                                                                                                             Q53VQ5_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=IGM;
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                                                                                                                   RESULT COSTON CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 VOLQESGPGLVKPSQSLSLTCSVTGYSITSGYFWNWIRQPPGNKLEWLGFIKYDGSNGYN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 PSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCA--RYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                 (alpha) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Gaps
                                                                                                                                                                                                     MEDLINE=79148758; PubMed=428562;
Schechter I., Wolf O., Zemell R., Burstein Y.;
"Structure and function of immunoglobulin genes and precursors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE REVISION TO 53.

MEDLINE=77244979; PubMed=268248;
Hood L., Margolies M.N., Givol D., Zakut R.;
Unpublishes Gresults, cited by:
Unpublishes Cresults D.R., Pecht I., Givol D., Wright C.;
Padlan B.A., Davies D.R., Pecht I., Givol D., Wright C.;
Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
-!- MISCELLANEOUS: This alpha chain was isolated from a myeloma
                                     Jilka R.L., Pestka S.; "Amino acid sequence of the precursor region of MOPC-315 mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heavy chain V region MOPC 315.
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6 -> GG (in Ref. 1; CAA30727).

G -> H (in Ref. 2).

GY -> YG (in Ref. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity-determining-1. Framework-2.
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Framework-4.
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=74170779; PubMed=4524622;
Francis S.H., Leelie R.G.Q., Hood L., Eisen H.N.;
Manino-acid sequence of the variable region of the heavy
of a mouse myeloma protein with anti-hapten activity.";
Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15399 MW; FB3828304C2B81DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein that has anti-dinitrophenyl activity.
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Missing (in Ref. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00406; IGv; 1.—
PROSITE; PSS0835; IG_LIKE; 1..
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Signal.
                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ensembl; ENSMUSG0000057048; Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M27638; AAA61337.1; -; Genomic DNA EMBL; X07880; CAA30727.1; -; Genomic_DNA
           MEDLINE=78094475; PubMed=414225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                         Fed. Proc. 38:1839-1845(1979)
                                                                                            chain.
                                                                                                                                                                                                                                                                                                                                                PROTEIN SEQUENCE OF 19-136.
                                                                                                                                                                             PROTEIN SEQUENCE OF 1-21.
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68
                                                                                         immunoglobulin heavy
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137
137 AA;
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P01822; 20-137
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Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A physins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A papleron M., Soares M.B., Bonaldo M.F., Carahnoi P., Forner A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carahnoi P., Frange C.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carahnoi P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan R.J., Malek J.A., Ghustarne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,
A Whiting M., Madan A., Young A., Sodergren E.J., Lu X., Glbbs R.A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.B.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.B.,
Bronerzelion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSETLSLTCTVSGYSITG-GYLWNWIRQPPGKGLEWMGYISYDGTNN 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 YKPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 YNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARLGMGAFDFWGHGTWVTVSS 137
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
and high-affinity monoclonal IgM and IgAl rheumatoid factors produced by CD5+ B cells from a rheumatoid arthritis patient."; Int. Immunol. 3:865-875(1991).

EMBL; AR107795; AR779084.1; -; mRNA.

PIR; $31673; $31673.

PIR; $31673; 20.447.

SMR; O95973; 20-147.

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

SMART; SM0406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 1.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.7%; Score 450.5; DB 2; Length 150; 73.7%; Pred. No. 1.7e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential.
VH4 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches 19; Indels
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20 >150 VH4 heavy chain variable 3
150 150 WW, 85664E04938AA7C9 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Best Local Similarity 73.7*
Matches 87; Conservative
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QEP418 HUMAN PRELIMINARY;
Q6P418;
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TISSUE=Primary B-Cells;
Strausberg R.;
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SIGNAL
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61 KPSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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A Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

L Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

B Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

B RHSP; PO1820; 147J.

B RHSP; PO1820; 147J.

B RHSP; PO1820; 147J.

B RHSP; PRO001010; 19-11ke.

InterPro; IPR00110; 19-11ke.

InterPro; IPR001596; 19-1.

INTERPRO; IPR001596; 10-1.

INTERPRO; IPR001596; 10-1.

INTERPRO; IPR001596; 10-1.

INTERPRO; IPR001596; 10-1.

INTERPRO; IPR001596; 10-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.7%; Score 450.5; DB 2; Length 576; 72.5%; Pred. No. 7.5e-38; artive 10; Mismatches 20; Indels 3
EMBL; BC063384; AAH63384.1; -; mRNA.

R HSRP; PO1820; 1A7N.

R Ensembl; BC060000196122; Homo sapiens.

R InterPro; IPR003599; Ig.

R InterPro; IPR003596; Ig.

R Fam; PF00047; Ig.

R SWART; SM00409; IG; 1.

R SWART; SM00409; IG; 1.

R SWART; SM00406; IG; 1.

R PROSITE; PS50395; IG LIKE; 4.

R PROSITE; PS50395; IG LIKE; 4.

R PROSITE; PS60399; IG. MHC; UNKNOWN 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686K04218 (Fragment)
Name=DKFZp686K04218;
Homo saplens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7Z379_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein
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115 VSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
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RX TISSURE-primary B-Cells,

RX TISSURE-primary B-Cells,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altechenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McReann P.J., McKernan K.J., Mallek J.A., Gunaratne P.H.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

RA Hakesley R.W., Touchman J.W., Green E.J., Dickson M.C.,

RA Butkesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

RA Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Generation and initial analysis of more than 15,000 full-length human

RA Mall N.S., A. Schein J.E., Jones S.J.M., Marra M.A.,

Rand Mouse C.DN sequences."

Rand Mouse C.DN sequences."

Rand Mouse C.DN sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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PubMed=1904154;

Naele G.A., Kitchingman G.R.;

Neale G.A., Kitchingman G.R.;

chain enhancer region contain a non-translatable exon and are
extremely heterogeneous at the 5' end.";

Nucleic Acids Res. 19:2427-2433(1991).

EMBL: BC011857; AANT1857.2; -; mRNA.

PIR; S15590; S15590.
   19 QVQLQESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQAPGRGLEWMGYIYYSGSTY
                                                                        60 YKPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCAR---YGRVFFDYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH MGC Project;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               620 AA
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SMR; Q96EYO; 27-251.
Ensembl; ENSG0000130076; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP07654; C1-set; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q96EYO HUMAN PRELIMINARY;
Q96EYO;
Q1-DEC-2001 (TrEMBLRel. 19, C:
01-DEC-2001 (TrEMBLRel. 19, L:
01-MAR-2004 (TrEMBLRel. 26, L:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Primary B-Cells;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                               S 117
                                                                                                                                                                                                                                                                                    S 138
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92 YSPSLKSRLTIFVDTSKNHFSLRLTSVTAADTAVYYCVRHVEGPYG--WFDPWGQGTLVT 149
                                                                                                                                                                                                                                                                                                                                                                                                                   61 KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCA----RYGRVFFDYWGQGTLVTVS 116
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Bukaryota, Merazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 YKPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCAR-----YGRVFFDYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Human rectum tumor;

A Flobe G., Han M., Weener H.W., Weil B., Amid C., Osanger A.,

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

L Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX538077; CAD98001.1; -; mRNA.

EMBL; BX538077; CAD98001.1; -; mRNA.

EMBL; BX53800701.10; Ig-1; ememb; ENSG00000130076; Homo sapiens.

R InterPro; IPR003596; Ig-1.

R InterPro; IPR003596; Ig-1.

R InterPro; IPR003596; Ig-1.

R FRAM; SM00406; IG-1.

R FRAM; SM00406; IG-1.

R PROSITE; PS50835; IG-1.

R PROSITE; PS508290; IG-MHC; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                       27 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPAGKGLEWIGRIYTSGSTNY
                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                          Length 620;
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69.4%; Score 436; DB 2; Length 49
Best Local Similarity 71.5%; Pred. No. 2e-36;
Matches 88; Conservative 9; Mismatches 18; Indels
                                                                                                                                                                                          70.6%; Score 443.5; DB 2; Length 75.2%; Pred. No. 4.3e-37; ative 6; Mismatches 19; Indels
SMART; SM00409; IG; 2.
SMART; SM00407; IGcl; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS50290; IG_MHC; UNKNOWN 3.
SEQUENCE 620 AA; 68125 MW; 990AlA4A6E8FF27B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686C02218 (Fragment)
Name=DKFZp68GC02218,
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                            Query Match
Best Local Similarity 75.2<sup>5</sup>
These 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q72374 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein
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150 VSS 152

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MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
"The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
EMBO J. 4:3681-3688 [1985].
                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 69.3%; Score 435.5; DB 2; Length 120; Best Local Similarity 68.1%; Pred. No. 4.8e-37; Matches 81; Conservative 15; Mismatches 14; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03375; CAA27077.1; -; mRNA.
EMBL; X03374; CAA27071.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 120
120 AA; 13892 MW; 013452306EBAA3BE CRC64;
                                                                                                                                                     13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
VH-D-JH region (Fragment).
Mus musculus (Mouse)
                                                                                120 AA
                                                                                PRT;
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NUCLEOTIDE SEQUENCE OF 28-29.
                                                                            Q53VR7 MOUSE PRELIMINARY;
Q53VR7;
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NON TER
SEQUENCE
                                        MOUSE
RESULT 15
CG53VR7 MOU
DG 53VR7 MOU
DG 53VR8
AC G53VR8
DT 13-SE
DT 13-SE
DT 13-SE
DT 13-SE
DE VH-D-
CC MURIS
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Search completed: January 10, 2006, 20:53:27 Job time : 79.8731 secs

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January 10, 2006, 20:55:23; Search time 5.96642 Seconds (without alignments) 166.558 Million cell updates/sec
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1 DVQLQBSGPGLVKPSQSLSL......RYGRVFFDYWGQGTTLTVSS 117
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cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
cgn2 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
cgn2 6/ptodata/1/pubpaa/USO3 NEW PUB.pep:*
cgn2 6/ptodata/1/pubpaa/USO3 NEW PUB.pep:*
cgn2 6/ptodata/1/pubpaa/USO1 NEW PUB.pep:*
cgn2 6/ptodata/1/pubpaa/USO1 NEW PUB.pep:*
cgn2 6/ptodata/1/pubpaa/USO1 NEW PUB.pep:*
GenCore version 5.1.6 (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                             61141 seqs, 8493638 residues
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                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                   Copyright
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	, App	4, Ap	2, Appli	_	8, Ap	Appl		, Appli	1651, Ap	Appl	Appl
g	. 69	52,	70,	75,	77,	79,	81,	34,	7,1,	49,	83,	85,	71,	22,	162,	1994,	7	1619,	1548,	73,	841,	4,	165	13,	18,
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	2-3	2-3	2-3	2-3	-012-353-7	-012-353-	2-3	1-7	12-1	12-1	-012-353-83	12-3	-012-353-7	-009-939-2	12-3	34-5	-185-615-2	34-5	34-5	-012-353-7	-054-515-841	35-6	-054-515-1	23-3	3-3
	11-012-353-6	1-01	11-012-353-7	11-012-353-75	1-01	1-01	1-0	10-512-184-	10-512-184-7	0-53	1-0	1-0	1-0	1-0	1-0	1-0	1-1	1-0	1-0	1-0	1-0	1-1	1-0	6-9	10-923-327-18
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% Query Match	100.0	100.0	89.5	85.8	85.8	85.1	85.1	84.8	84.8	4.8	83.2	83.2	78.2	6.8	73.4	6.4	64.2	3.7	63.3	5.9	2.7	62.4	2.2	62.1	2.1
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Sequence 7, Appli Sequence 9, Appli Sequence 13.9, Appl Sequence 1361, Ap Sequence 1. Appli Sequence 15.8, Ap Sequence 15.8, Ap Sequence 1981, Ap Sequence 100, Appl Sequence 100, Appl Sequence 17, Appli Sequence 25, Appl Sequence 66, Appl Sequence 66, Appl Sequence 167, Appl	Sequence 11, Appl Sequence 1960, Ap
US-10-923-327-7 US-11-012-353-72 US-11-012-353-72 US-11-054-515-1361 US-11-054-515-1361 US-11-054-515-1361 US-11-054-515-1981 US-11-054-515-1981 US-11-054-515-1987 US-11-054-515-1987 US-11-054-515-1987 US-11-054-515-1007 US-11-054-515-1007 US-11-128-900-7 US-11-128-900-86 US-10-923-327-14 US-10-923-327-19	US-10-923-327-11 US-11-054-515-1960
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## ALIGNMENTS

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TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 01773-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT PILING DATE: 2004-12-16

PRIOR APPLICATION NUMBER: RR 0308538

PRIOR APPLICATION NUMBER: FR 0308538

PRIOR APPLICATION NUMBER: FR 0308538

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-20

PRIOR FILING DATE: 2003-07-10

PRIOR FILING DATE: 2000-07-20

PRIOR FILING DATE: 2000-07-20

PRIOR FILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 162

SOFTWARE: PatentIn Ver. 3.3
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100.0%; Pred. No. 8.9e-51;
tive 0; Mismatches 0;
              Sequence 69, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
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Best Local Similarity 100.
Matches 117; Conservative
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US-11-012-353-69
US-11-012-353-69
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SEQ ID NO 75
LENGTH: 117
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US-11-012-353-52

Sequence 52, Application US/11012353

Sequence 52, Application US/11012353

Sequence 52, Application No. US20050249730A1

SERENAL INFORMATION:

APPLICANT: GORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: LEGER, OLIVIER

APPLICANT: LEGER, OLIVIER

APPLICANT: LEGER, OLIVIER

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

FILE REPERENCE: 01773-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT APPLICATION NUMBER: PR 0204-12-16

FRIOR PRIOR PLIING DATE: 2003-07-11

FRIOR PLIING DATE: 2003-07-11

FRIOR PLIING DATE: 2003-01-20

FRIOR PLIING DATE: 2003-01-20

FRIOR PLIING DATE: 2002-01-18

FRIOR PLIING DATE: 2002-01-18

FRIOR PLIING DATE: 2002-01-18

FRIOR PLIING DATE: 2002-01-18

FRIOR FILING DATE: 2003-01-20

FRIOR FILING DATE: 2002-01-18

FRIOR FILING DATE: 2003-01-20

FRIOR FILI
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Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DUFLOS, ALAIN

APPLICANT: BECK, ALAIN

APPLICANT: BECK, ALAIN

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: RECEFTORS ANTIBODIES AND USES THEREOF

FILE REFRENCE: 017753-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT PLING DATE: 2004-12-16

PRIOR PLING DATE: 2003-07-11

PRIOR PLING DATE: 2003-07-11

PRIOR PLING DATE: 2003-07-07

PRIOR FILING DATE: 2003-01-20

PRIOR APPLICATION NUMBER: FC 7PR03/00178
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US-11-012-353-52
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SEPELCANT: GOETSCH, LILIANE
APPLICANT: GOETSCH, LILIANE
APPLICANT: CORVAIA, NATHALIB
APPLICANT: CORVAIA, NATHALIB
APPLICANT: CORVAIA, NATHALIB
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPPORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 020653
PRIOR FILING DATE: 2002-01-18
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PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PatentIn Ver. 3.3
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US-11-012-353-75

i Sequence 75, Application US/11012353
i Publication No. US20050249730A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 3.3
                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Mus musculus
US-11-012-353-70
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US-11-012-353-75
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Query Match
Best Local Similarity 84.51
Matches 98, Conservative
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SEQ ID NO 81
                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-11-012-353-79
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                                                                                                                                                                                                            LENGTH: 117
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              Sequence 77, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
TITLE OF INVENTION: NOVEL ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
FRIOR PELING DATE: 2004-12-16
FRIOR PELING DATE: 2003-01-10
FRIOR PELING DATE: 2003-01-20
FRIOR PELING DATE: 2002-01-18
FRIOR FILING DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGEN, OLLVIER
APPLICANT: LEGEN, OLLVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGP-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NCFEPTORS ANTIBODIES AND USES THEREOF
TILLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REPERENCE: 01775-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR RELING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR FILING DATE: 2003-07-11
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86.2%; Pred. No. 1.1e-42;
tive 8; Mismatches 8
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; Sequence 79, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
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Best Local Similarity 86.2
Matches 100; Conservative
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; ORGANISM: Homo sapiens
US-11-012-353-77
US-11-012-353-77
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GENERAL INCORNATION:

GENERAL INCORNATION:

APPLICANT: GORVAIA, NATHALIB

APPLICANT: CORVAIA, NATHALIB

APPLICANT: CORVAIA, NATHALIB

APPLICANT: DUFLOS, ALAIN

APPLICANT: HAEUW, JEAN-FRANCOIS

APPLICANT: HEEEK, OLIVIER

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-198

CURRENT APPLICATION NUMBER: 10/735,916

PRIOR APPLICATION NUMBER: 10/735,916

PRIOR APPLICATION NUMBER: PR 0308538

PRIOR PLILING DATE: 2003-07-11

PRIOR PLILING DATE: 2003-07-11

PRIOR PLILING DATE: 2002-05-07

PRIOR PLILING DATE: 2002-05-07

PRIOR FILING DATE: 2002-05-07

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.1%; Score 541; DB 7;
84.5%; Pred. No. 2.7e-42;
rative 10; Mismatches 8.
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR PELLING DATE: 2002-05-07
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER: OF SEQ ID NOS: 162
SOFTWARR: PATENTING PATE: 2002-01-18
SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 81, Application US/11012353; Publication No. US20050249730A1; GENERAL INFORMATION:
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SQUEENCE 83, Application US/11012353

SQUEENCE 83, Application US/11012353

SENERAL INPORMATION:
APPLICANT: CORVAIA, NATHALIB
APPLICANT: CORVAIA, NATHALIB
APPLICANT: CORVAIA, NATHALIB
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPPORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPPORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPPORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION NUMBER: US/11/012/353
CURRENT FILING DATE: 2004-12-16
PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
115 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYISYDGTNNN 174
                                                                                                          RESULT 10

US-10-512-184-49

US-10-512-184-49

US-10-512-184-49

Sequence 49, Application US/10512184

Publication No. US20050244901A1

GENERAL INFORMATION:

APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung in TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant in TITLE OF INVENTION: resistance against fungi current application NUMBER: US/10/512,184

CURRENT PILING DATE: 2004-10-22

CURRENT PILING DATE: 2004-10-22

SOPTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 NPSLKNRISITRDASKNQFFLKINSVTTEDTATYHCARGAPYYGKGTWFPYWGQGTLVTV
                                                                            KPSLKDRISITRDTSKNQPFLKLNSVTNEDTATYYCAR----YGR-VFFDYWGQGTTLTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: fusion protein OTHER INFORMATION: comprising the leader peptide - chitinase- linker OTHER INFORMATION: - scFv PL2 - cmyc/His6.
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Pred. No. 1.8e-41;
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Matches 103; Conservative
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US-10-512-184-49
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US-11-012-353-83
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                                                                                                                    Sequence 34, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SEQ ID NOS: 72
SEQ ID NO 71
LENGTH: 371
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     PSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with OTHER INFORMATION: specificity against Phoma lingam; originates from OTHER INFORMATION: Mus musculus.
US-10-512-184-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 84.8%; Score 539.5; DB 6; Best Local Similarity 84.4%; Pred. No. 7.8e-42; Matches 103; Conservative 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 71, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 34
LENGTH: 259
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                                                                                  RESULT 8
US-10-512-184-34
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96; Conservative
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US-11-012-353-71
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Best Local Similarity
Matches 96; Conserv
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US-11-012-353-85

j Sequence 85, Application US/11012353

j Sequence 86, Application WS/11012353

j Dublication No. US20050249730A1

j GENERAL INFORMATION:

j APPLICANT: GORTSCH, LILIANE

j APPLICANT: DUFLOS, ALAIN

APPLICANT: HEREW, JENN-FRANCOIS

APPLICANT: ALAIN

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-198

CURRENT FILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: FR 0200653

PRIOR APPLICATION NUMBER: FR 0200653

PRIOR APPLICATION NUMBER: FR 0200654

PRIOR FILING DATE: 2002-01-18

SOFTWARE: PRIOR PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 PSLKORVIISVDISKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
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82.8%; Pred. No. 3.7e-41;
ive 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 83.2%; Score 529; DB 7; Length 117; Best Local Similarity 82.8%; Pred. No. 3.2e-41; Matches 96; Conservative 11; Mismatches 9; Indels
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR FILING DATE: 2003-01-20
PRIOR PELLING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 020553
PRIOR PLILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
SEQ ID NOS: 162
SOFTWARE: PATENTIN VET. 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-83
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Best Local Similarity
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US-11-01-255-71

US-11-01
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Sequence 162, Application US/11012353

Sequence 162, Application Ws/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: BAUGOS, ALAIN

APPLICANT: LEGEN, OLIVIER

APPLICANT: BEEK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFRERCE: 017753-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT FILING DATE: 2004-12-16

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2002-01-20

PRIOR FILING DATE: 2002-01-18

NUMBER: PATCHTING DATE: 2002-01-18

PATCHTING DATE: 2002-01-18

NUMBER: PATCHTING DATE: 2002-01-18

PATCHTING DATE: 2002-01-18
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                                                                                                                                                                                                                                                         7; Gaps
                                                                                                                                                                          76.8%; Score 488.5; DB 7; Length 118; 76.9%; Pred. No. 1.3e-37; Live 9; Mismatches 12; Indels 7;
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                                                                                                                                                                          Query Match
Best Local Similarity 76.9°
Matches 93; Conservative
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-22
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ORGANISM: Homo sapiens
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US-11-012-353-162
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Search completed: January 10, 2006, 21:36:23 Job time : 5.96642 secs

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61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
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US-10-735-916A-52
Sequence 52, Application US/10735916A
; Publication No. US20050084906A1
TYPE: PRT
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81, Appl
83, Appl
85, Appl
119, App
25, Appl
26, Appl
260, Appl
270, Appl
54, Appl
                                                                                                                                                                                                                        January 10, 2006, 20:53:43; Search time 64.1754 Seconds (without alignments) 761.757 Million cell updates/sec
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636
1 DVQLQESGPGLVKPSQSLSL......RYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 69,
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Sequence
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USIO8_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USIO8_PUBCOMB.pep:*

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                                 5.1.6
Compugen Ltd
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US-10-735-916A-52
US-10-735-916A-70
US-10-735-916A-75
US-10-735-916A-75
US-10-735-916A-75
US-10-735-916A-79
US-10-735-916A-79
US-10-735-916A-81
US-10-735-916A-81
US-10-735-916A-82
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US-10-632-706-67
US-10-741-657A-21
US-09-791-551-109
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                                     GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Perfect score:
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Sequence 69, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:
APPLICANT: GORYSCH, Liliane
APPLICANT: CORVALA, Nathalie
APPLICANT: UEGER, Ollyier
APPLICANT: DEGER, Ollyier
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
ITILE REPERENCE: 017755-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
FRIOR APPLICATION NUMBER: PR 03/08 538
FRIOR APPLICATION NUMBER: PR 02/06 653
FRIOR APPLICATION NUMBER: FR 02/06 654
FRIOR PILING DATE: 2002-01-18
FRIOR PILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 69:
SEQ ID NO 69:
TENGRAL 11-11
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US-10-184-300A-3

US-09-920-171-2

US-10-113-996-2

US-10-791-619-2

US-09-802-077-3

US-09-802-077-3

US-09-802-077-3

US-09-802-179-3

US-10-968-237-3

US-10-173-248-7

US-10-741-657A-19

US-10-741-657A-19

US-10-308-817-131

US-10-816-938-29

US-10-310-674A-36

US-10-310-674A-36
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US-10-735-916A-70
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US-10-735-916A-70

Sequence 70, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:

APPLICANT: GOTSCH, Liliane

APPLICANT: CORYDAL, Nathalie

APPLICANT: EEGER, Olivier

APPLICANT: BECK, Alain

APPLICANT: HAEUW, Jean-Francois

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 01733-183

CURRENT APPLICATION NUMBER: RR 03/08 538

FRIOR PELLING DATE: 2003-12-16

PRIOR PELLING DATE: 2003-07-18

PRIOR APPLICATION NUMBER: PR 02/00 653

PRIOR APPLICATION NUMBER: PR 02/00 653

PRIOR APPLICATION NUMBER: PR 02/00 654

PRIOR PILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                APPLICANT: CORVESCH, DILIAGUE
APPLICANT: CORVESCH, DILIAGUE
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Alain
APPLICANT: BECK, Alain
APPLICANT: HARUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 01773-183
CURRENT FILING DATE: 2003-12-16
PRIOR PLILING DATE: 2003-01-20
PRIOR PLILING DATE: 2003-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR PLILING DATE: 2002-01-18
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100.0%; Score 636; DB 5;
Best Local Similarity 100.0%; Pred. No. 4.9e-51;
Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-52
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ORGANISM: Mus musculus
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| Sequence 117, Application US/10372481
| Sequence 117, Application US/030202975A1
| Publication No. US20030202975A1
| GENERAL INFORMATION:
| APPLICANT: Tedder, Thomas F.
| TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
| FILE REFERENCE: 5405.306
| CURRENT PILING DATE: 2003-02-21
| FRIOR APPLICATION NUMBER: US/10/372,481
| PRIOR FILING DATE: 2003-02-21
| PRIOR FILING DATE: 2003-02-21
| PRIOR FILING DATE: 2002-10-21
| PRIOR FILING DATE: 2002-10-21
| PRIOR PLICATION NUMBER: US 60/420,472
| PRIOR FILING DATE: 2002-10-21
| PRIOR PLICATION NUMBER: US 60/359,419
| PRIOR PLICATION NUMBER: 31
| SOFTWARE: PatentIn version 3.2
| SOFTWARE: PatentIn version 3.2
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Bublication No. US2004001828A1

GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: TEXTEDER, Thomas

TITLE OF INVENTION: TREATHENINT METHODS USING ANTI-CD22

TITLE OF INVENTION: ANTIHEODIES

FILE REFERENCE: 39754-0951

CURRENT FILING DATE: 2003-02-11

PRIOR FILING DATE: 2003-02-11

PRIOR FILING DATE: 2002-10-21

PRIOR FILING DATE: 2002-10-21

PRIOR FILING DATE: 2002-02-21

PRIOR FILING DATE: 2002-02-21

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PSECSEC for Windows Version 4.0

SEQ ID NO 17

LENGTH: 118
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                                                       Indels
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Pred. No. 5.5e-43;
5; Mismatches 9;
     DB 5;
  Score 569.5; DB 5;
Pred. No. 6.4e-45;
2; Mismatches 8;
  89.5%;
ilarity 90.7%;
Conservative 2
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Best Local Similarity 87.3%;
Matches 103; Conservative
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US-10-372-481-17
Query Match
Best Local Similarity
Matches 107; Conserv
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RESULT 9
US-10-735-916A-79
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                                                                                                                                                                                                                     61 NPSLKARISITRDISKNOFFLKINSVTTEDTATYYCARGGITVAMDYWGQGTSVTVSS 118
                                                                                                                                                                                                    61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCARYG-RVFPDYWGQGTTLTVSS 117
                                                                                                                                  1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
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                                                                                                    1; Gaps
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                                                                                                                                                                                                                                                                                                                   Sequence 75, Application US/10735916A
Publication No. US20050084906A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
                                                                 Query Match 86.2%; Score 548.5; DB 4; Length 118; Best Local Similarity 87.3%; Pred. No. 5.5e-43; Matches 103; Conservative 5; Mismatches 9; Indels 1
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85.8%; Score 546; DB 5;
Best Local Similarity 86.2%; Pred. No. 9.4e-43;
Matches 100; Conservative 8; Mismatches 8.
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Publication No. US20050084906A1
GRERAL INFORMATION:
APPLICANT: GOSTSCH, Liliane
APPLICANT: LORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
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ORGANISM: Homo sapiens
US-10-735-916A-75
; TYPE: PRT; ORGANISM: homo sapiens US-10-371-797-17
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US-10-735-916A-77
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Sequence 2, Application US/09858349
Patent No. US20020012909A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SMALL FUNCTIONAL UNITS OF ANTIBODY HEAVY CHAIN VARIABLE REGIONS
FILE REFERENCE: 87534-2800
CURRENT APPLICATION NUMBER: US/09/858,349
CURRENT FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
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APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REPREMENT
CURRENT APPLICATION NUMBER: US/10/735, 916A
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: R 03/08 538
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR PLING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-18
PRIOR PLING DATE: 2003-01-18
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTING VET. 2.1
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ORGANISM: mouse hybridoma specific for H-2D + RGPGRAFVTI peptide
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ORGANISM: Homo sapiens
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LENGTH: 135
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LENGTH: 136
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, ORGANISM: Homo sapiens
US-10-735-916A-81
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  TYPE: PRT
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                                    HUBLICARTION NO. US20050084906A1

APPLICANT: GOETSCH, Liliane
APPLICANT: GOETSCH, Liliane
APPLICANT: GOETSCH, Liliane
APPLICANT: USGRA, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, JOHN-Francois
FILE OF INVENTION: NOWBER: US/10/735,916A
CURRENT APPLICATION NUMBER: FR 03/08 538
PRIOR APPLICATION NUMBER: FR 03/08 538
PRIOR APPLICATION NUMBER: FR 02/06 653
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/06 653
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/06 654
PRIOR APPLICATION NUMBER: FR 02/06 654
PRIOR APPLICATION NUMBER: FR 02/05 753
PRIOR APPLICATION NUMBER: FR 02/05 753
PRIOR APPLICATION NUMBER: FR 02/05 753
PRIOR PILING DATE: 2002-01-18
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Best Local Similarity 84.5%; Pred. No. 2.7e-42;
Matches 98; Conservative 10; Mismatches 8
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Sequence 79, Application US/10735916A
Publication No. US20050084906A1
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 81
LENGTH: 135
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US-10-735-916A-79
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61 KPSLKDRISITRDTSKNQPPLKLNSVTNEDTATYYCAR-YGRV--PFDYWGQGTTLTVSS 117
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                                                                                                                        2 VOLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK
                                                                                                                                                                                                                                        62 PSLKDRISITRDISKNQFFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                      80 PSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 135
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                                                               Gaps
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Sequence 83, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES
CURRENT APPLICATION WUMBER: US/10/735,916A
CURRENT PILING DATE: 2003-12-16
PRIOR APPLICATION WUMBER: PRO3/00 178
PRIOR APPLICATION WUMBER: PCT/FR 03/00 178
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Pred. No. 5.6e-41;
6; Mismatches 10; Indels 3:
Query Match

85.1%; Score 541; DB 5; Length 135;
Best Local Similarity 84.5%; Pred. No. 3.1e-42;
Matches 98; Conservative 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LIAME, TONY W.
APPLICANT: LIAME, TONY W.
APPLICANT: LOO, Deryk T.
TITLE OF INVENTION: KID3 AND KID3 ANTIBODIES THAT BIND
TITLE OF INVENTION: THERETO
FILE REFERENCE: 415072002700
CURRENT FILING DATE: 2004-09-17
PRIOR APPLICATION NUMBER: US 60/504,441
PRIOR APPLICATION NUMBER: US 60/504,441
PRIOR FILING DATE: 2003-09-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 4, Application US/10943640; Publication No. US20050152907A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.2%;
Matches 101; Conservative 6
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial
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; ORGANISM: Mus sp.
US-09-791-551-119
                                                                 JS-09-791-551-119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VOLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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US-10-735-916A-85
; Sequence 85, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
   APPLICANT: GORTSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECER, Olivier
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: UOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 83.2%; Score 529; DB 5; Length 135; Best Local Similarity 82.8%; Pred. No. 4e-41; Matches 96; Conservative 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 83.2%; Score 529; DB 5; Length 117; Best Local Similarity 82.8%; Pred. No. 3.5e-41; Matches 96; Conservative 11; Mismatches 9; Indels
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CURRENT FILING DATE: 2003-12-16
PRIOR PAPLICATION NUMBER: ER 03/08 538
PRIOR FILING DATE: 2003-07-11
PRIOR PELING DATE: 2003-07-11
PRIOR PELING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR FILING DATE: 2002-01-18
PRIOR PRIOR PRING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PRILING DATE: 2002-01-18
PRIOR PRILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 83
LENGTH: 117
TYPE: PRT
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US-10-735-916A-85
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Sequence 2, Application US/10383447
; Sequence 2, Application US/10383447
; Publication No. US20040096392A1
; Geberral Information:
; APPLICANT: Bhaskar, Vinay
; APPLICANT: Caras, Ingrid
; APPLICANT: Caras, Ingrid
; APPLICANT: Ramakrishnan, Vanitha
; APPLICANT: Ramakrishnan, Vanitha
; APPLICANT: Anakrishnan, Vanitha
; TITLE OF INVENTION: Antibodies Against Cancer Antigen TMEFF2 and Uses Thereof
; FILE REFERENCE: 05882.0138.NPUSO0
; CURRENT FILING DATE: 2002-03-07
; FRIOR APPLICATION NUMBER: US 60/362,837
; PRIOR APPLICATION NUMBER: US 60/463,812
; PRIOR FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 34
; FRANTH: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCARYGRVF------FDYWGQGTTL 113
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Sequence 119, Application US/09791551

Publication No. US20030235584A1

Bublication No. US20030235584A1

GENERAL INFORMATION:

APPLICANT: KLOSTZER, WILLIAM S.

APPLICANT: HANNA, NABIL

TILL OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES

FILE REFERENCE: 037003/02778B5

CURRENT FILING DATE: 2001-02-26

PRIOR PELLING DATE: 2000-02-28

PRIOR FILING DATE: 2000-02-28

PRIOR FILING DATE: 2000-03-28

PRIOR FILING DATE: 2000-03-8

PRIOR FILING DATE: 2000-03-8

PRIOR FILING DATE: 2000-03-18

NUMBER OF SEQ ID NOS: 119

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.2%; Score 522.5; DB 3; Length 144; Best Local Similarity 78.2%; Pred. No. 1.7e-40; Matches 97; Conservative 10; Mismatches 10; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.0%; Score 521.5; DB 4; Length 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Search completed: January 10, 2006, 21:35:32 Job time : 65.1754 secs Sequence 101, App Sequence 10, Appl Sequence 11, Appl

7, Appli 7, Appli 7, Appli 13, Appli 13, Appli 13, Appli 2, Appli 14, Appli 10, Appli 11, Appli

Sequence Sequence Sequence 1

Sequence Sequence

Sequence

Sequence 13, Sequence 13, Sequence 13,

Sequence Sequence Sequence Sequence Sequence Sequence

Perfect score:

Sequence:

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Scoring table:

Searched:

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2 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK
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ZIP: 22314

ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-00S/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: P-42,368
REGISTRATION NUMBER: 9-42,368
REGISTRATION NUMBER: 50356-151
TELEFROWNICATION INFORMATION:
TELEFRAM: 703-518-5100
TELEFRAM: 703-518-5100
TELEFRAM: 703-518-5100
TELEFRAM: 703-518-5100
TELEFRAM: 103-518-5100
TELEFRAM: 103-518-5100
TELEFRAM: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: SEINO, Ken-ichiro
APPLICANT: SEINO, Ken-ichiro
APPLICANT: YAGITA, Hideo
APPLICANT: YAGITA, Hideo
APPLICANT: OKUMURA, Ko
APPLICANT: OKUMURA, Ko
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
US-08-436-717-31

US-08-466-151-7

US-08-466-1538-7

US-09-802-096-7

US-09-922-179-7

US-09-214-095D-13

US-09-214-095D-13

US-09-214-095D-13

US-09-345-114

US-09-345-114

US-09-345-114

US-08-672-345C-10

US-08-672-345C-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: McDermott, Will & Emery
STREET: 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09065059 Patent No. 6068841
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US-09-065-059-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 3, A Se
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636
1 DVQLQESGRGLVKPSQSLSL.....RYGRVPFDYWGQGTTLITVSS 117
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FCOMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-109-207C-2
US-09-920-105-2
US-09-920-111-2
US-09-920-111-2
US-09-920-111-2
US-09-920-115-3
US-09-802-096-3
US-09-802-096-3
US-09-802-096-3
US-08-902-486-15
US-08-902-95-179-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -08-308-494A-13
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US-08-137-117D-31
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Database :

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                                                                                                                                                                                                                                                                                                   APPLICANT: KAYAGAKI, No. 6946255uhiko
APPLICANT: YAGITA, Kideo
APPLICANT: YAGITA, Kideo
APPLICANT: YAGITA, Ko
APPLICANT: WAKATA, Motomi
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: REACTING WITH FAS LIGAND AND PRODUCTION PROCESS THEREOF
TITLE OF INVENTION: REACTING WITH FAS LIGAND AND PRODUCTION PROCESS THEREOF
TITLE OF INVENTION: ADDRESS:
ADDRESSE: MCDERMOUT, Will & Emery
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
1 VOLOESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYISYDGSNNYN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,555
FLING DATE: 19-5EP-1997
CLASSIPICATION: 530
ATTORNBY AGENT INFORMATION:
NAME: Bucca Ph.D., Daniel
REGISTRATION NUMBER: 42,3666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50356-150
                                                                                                                                                                                                                              Sequence 11, Application US/08913555
Patent No. 6946255
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPERENCE/DOCKET NUMBER: 5035
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-756-8600
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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Sequence 18, Application US/08767128
Patent No. 611079
GENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: WIRRAY, PETER JOSEPH
APPLICANT: GOBBEL, PETER

US-08-767-128-18

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Sequence 2, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-19E Antibodies and Method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCARCGNYPWYFDYWGQGTTLIVSS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISYSGSTSY
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                                                                                                                                                                           ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 84.9%; Score 540; DB 2; Length 119; Best Local Similarity 84.9%; Pred. No. 1e-49; Matches 101; Conservative 5; Mismatches 11; Indels
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMP
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LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 612/332-9081
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FRAGMENT TYPE: i
ORIGINAL SOURCE:
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US-08-887-352B-2
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptides FILE REFERENCE: Pli2SC1r
CURRENT PPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER APPLICATION NUMBER: US 08/887,352
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 2
                                                                   61 KPSLKDRISITRDISKNOFFLKLNSVTNEDTATYYCAR----YGRVFFDYWGQGTTLTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NPSLKNRISVTRDTSQNQFFLKLNSATAEDTATYYCARGSHYFGHWHFAVWGAGTTVTVS 120
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1 DVQLQESGPGLVKPSQSLSLACSVTGYSITSGYSWNWIRQFPGNKLEWMGSITYDGSSNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lowman, Henry B.
APPLICANT: Downan, Henry B.
APPLICANT: Downan, Henry B.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John B.
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
FILE REFERENCE: P1123C2US
CURRENT APPLICATION NUMBER: US/09/920,171
CURRENT PILING DATE: 2001-08-01
FRIOR APPLICATION NUMBER: US 08/887,352
FRIOR APPLICATION NUMBER: US 09/296,005
FRIOR APPLICATION NUMBER: US 09/296,005
FRIOR PILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
SEQ ID NOS: 44
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                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09296005
Patent No. 6290957
GENERAL INFORMATION:
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Best Local Similarity 79.3'
Matches 96; Conservative
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US-09-296-005-2
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ORGANISM: Mus
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Squence Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1
CURRENT FPLING DATE: 1998-06-30
PRIOR APPLICATION UNMBER: US 60/051,554
PRIOR APPLICATION UNMBER: US 60/051,554
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 2
LENGTH: 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
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Pred. No. 1.2e-46;
8; Mismatches 13; Indels
                                                                                                                                                                             COUNTY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winheatin (Genettech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SVODGAM: Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91,044
REFERENCE/DOCKET NUMBER: 9123
TELLEPHONE: 650/225-1489
TELLEPHONE: 121 amino acide
TYPE: Amino acide
  TITLE OF INVENTION: Improving Polypeptides NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 79.3%;
Matches 96; Conservative
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Best Local Similarity 79.34
Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: Linear
US-08-887-352B-2
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Query Match

1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY 60

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61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCAR----YGRVFFDYWGQGTTLTVS 116
                                                                                                                                                                                                                                                                                                                                                                       61 NPSLKNRISVTRDTSQNQFFLKLNSATAEDTATYYCARGSHYFGHWHFAVWGAGTTVTVS 120
                                                                                                                                                                                                                                                                               1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                               4.
                                                                                                                                                        Score 511; DB 2; Length 121;
Pred. No. 1.2e-46;
8; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
ADDRESSEE: Genentech, Inc.
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P0718P2C1D1
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/165899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 07/744768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3, Application US/08466151; Patent No. 6037453
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ATTORNEY/AGENT INPORMATION:
NAME: SYODOGA, Craig G,
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                          ch 80.3%;
1 Similarity 79.3%;
96; Conservative 8
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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  NUMBER OF SEQ ID NOS: 44
                                                                                          ; ORGANISM: Mus musculus
US-10-113-996-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
                                                                                                                                                             Query Match
Best Local Similarity
Matches 96; Conserv
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                       SEQ ID NO 2
LENGTH: 121
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US-08-466-151-3
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                                                                       TYPE: PRT
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
CURRENT APPLICATION NUMBER: US/09/716,028
PRIOR APPLICATION NUMBER: US 09/109,207
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-30
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                                                                                                                                                                  61 KPSLKDRISITRDTSKNOFFLKLNSVTNEDTATYYCAR----YGRVFFDYWGQGTTLTVS 116
                                                                                                                                                                                       61 NPSLKORISVTRDTSQNQFFLKLNSATAEDTATYYCARGSHYFGHWHFAVWGAGTTVTVS 120
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                            4; Gaps
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  79.3%; Pred. No. 1.2e-46;
tive 8; Mismatches 13; Indels
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APPLICANT: Dardieu, Paula M.
APPLICANT: Lowe, John
TILLE OF INVENTION: Improved Anti-IgE Antibodies
FILE REBERGE: P1123G3US
CURRENT APPLICATION NUMBER: US/10/113,996
CURRENT FILING DATE: 2002-04-01
PRIOR PELING DATE: 1997-07-02
PRIOR PELING DATE: 1997-07-02
PRIOR PELING DATE: 1999-04-21
PRIOR PELING DATE: 1999-04-21
PRIOR PELING DATE: 1099-04-21
PRIOR PELING DATE: 2001-08-01
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Patent No. 6761889
GENERAL INFORMATION:
APPLICANT: Lowman, Henry B.
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Patent No. 6723833
Best Local Similarity 79.34
Matches 96; Conservative
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SEQ ID NO 2
LENGTH: 121
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; ORGANISM: Mus musculus
US-09-716-028-2
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61 KPSLKDRISITRDTSKNOPPLKLNSVTNEDTATYYCAR----YGRVPFDYWGQGTTLTVS 116
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APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Peesta, Leonard G.
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
FILE REFERENCE: P0718P2C2US
CURRENT APPLICATION NUMBER: US/09/802,077
CURRENT FILING DATE: 1994-01-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR PILING DATE: 1994-01-26
PRIOR PLING DATE: 1994-01-26
PRIOR PAPLICATION NUMBER: US 07/879,495
PRIOR PAPLICATION NUMBER: US 07/879,495
PRIOR PPLING DATE: 1992-08-14
PRIOR PLING DATE: 1992-08-14
PRIOR PILING DATE: 1991-08-14
PRIOR PILING DATE: 1991-08-14
SHOR PILING DATE: 1991-08-14
SHOR PILING DATE: 1991-08-14
SEQ ID NOS: 64
SEQ ID NOS: 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Mismatches
CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR PLICATION NUMBER: US 08/185,899
PRIOR PLICATION NUMBER: PCT/US92/06860
PRIOR PLICATION NUMBER: PCT/US92/06860
PRIOR PELING DATE: 1992-08-14
PRIOR PLICATION NUMBER: US 07/879,495
PRIOR PLICATION NUMBER: US 07/879,495
PRIOR PLICATION NUMBER: US 07/879,795
PRIOR FILING DATE: 1992-05-07
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Matches 96; Conservative
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Matches 96; Conservative
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SEQ ID NO 3
LENGTH: 134
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US-09-802-077-3
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US-09-802-096-3
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US-09-802-077-3
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Patent No. 6685939
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
FILE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended FILE REPERBNCE: P0718P2C3US
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Pred. No. 1.4e-46;
8; Mismatches 13; Indels
                                                                                                           Length 134;
                                                                                                           80.3%; Score 511; DB 2; Length 13·79.3%; Pred. No. 1.4e-46; ive 8; Mismatches 13; Indels
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APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: PO718P2C1D1
CURRENT PAPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-03-16
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-16
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR PILING DATE: 1992-05-07
PRIOR PILING DATE: 1992-06-07
PRIOR PILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
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Best Local Similarity 79.3%;
Matches 96; Conservative
                                                                                                      Query Match
Best Local Similarity 79.3°
Matches 96; Conservative
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             Amino Acid
                               ; TOPOLOGY: Linear
US-08-466-151-3
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US-08-466-163B-3
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Search completed: January 10, 2006, 20:58:04 Job time : 23.847 secs
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61 KPSLKDRISITRDTSKNOFFLKLNSVTNEDTATYYCAR----YGRVFFDYWGQGTTLTVS 116
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APPLICANT: Russel, David R.

APPLICANT: Fuller, James T.

TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: ADDRESS:

ADDRESSEE: ADDRESSE:

ATREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.

APPLICANT: Jardieu, Leonard G.

TITLE OF INVENTION: Anti-TgE Antibodies (as amended)
FILE REFERENCE: POT18PZCIDICIUS
CURRENT FILICATION NUMBER: US/09/925,179

FRIOR APPLICATION NUMBER: US 08/46,163

PRIOR APPLICATION NUMBER: US 08/46,163

PRIOR APPLICATION NUMBER: US 08/465,617

PRIOR APPLICATION NUMBER: US 08/465,617

PRIOR APPLICATION NUMBER: US 08/185,899

PRIOR FILING DATE: 1994-01-26

PRIOR FILING DATE: 1992-08-16

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1992-08-14

PRIOR APPLICATION NUMBER: US 07/744,768

PRIOR SEQ ID NOS: 68

NUMBER OF SEQ ID NOS: 68
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US-08-902-486-13
Sequence 13, Application US/08902486
Patent No. 6140075
                                                                                                                                                                                                                                                        Sequence 3, Application US/09925179
Patent No. 6914129
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ZIP: 53701-2113
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-925-179-3
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Madison
STATE: WI
                                                                              S 117
                                                                                                                              s 121
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190 TPSLKNRVSITRDTSMNQFFLRLTSVTPEDTATYYCAR----LDYWGQGTSVTVSS 241
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                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,486
FILING DATE:
CLASSITCATION NUMBER: US/08/902,486
FILING DATE:
NAME: SGRY INFORMATION:
NAME: SGRY INFORMATION:
NAME: SCRY INFORMATION:
TELECOMMUNICATION NUMBER: 670513.90261
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1900
TELECOMMUNICATION 1900
                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-902-486-13
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## ALIGNMENTS

2443163

of hits satisfying chosen parameters: 2443163 segs, 439378781 residues

Total number

Searched:

Scoring table:

score:

Title: Perfect (

Sequence:

protein

Run on: δ

seq length: 0 seq length: 200000000

08 08

Minimum | Maximum |

insulin-like growth factor-l receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR. cytostatic; antipsoriatic; antibody; ADJ76903 standard; protein; 117 AA Anti-IGF-1R related protein #16. (first entry) 06-MAY-2004 ADJ76903; ADJ76903 

WO2003059951-A2 Homo sapiens.

24-JUL-2003

20-JAN-2003; 2003WO-FR000178

18-JAN-2002; 2002FR-0000653. 18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-0005753.

(FABR ) FABRE MEDICAMENT SA PIERRE.

Leger O; Corvaia N, ij Goetsch

WPI; 2003-569653/53.

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

Disclosure; SEQ ID NO 69; 164pp; French.

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or rear diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (IGFR) and/or epidermal growth factor receptor (IGFR) and/or epidermal growth factor receptor (IGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of

summaries geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su geneseqp2004s:* geneseqp2005s:* geneseqp1980s:* A Geneseq 1: qeneseq Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		de			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
	) ;					
н	636	100.0	117	7	ADJ76903	
7	636	100.0	117	σ	ADZ67073	Adz67073 Murine im
m	636	100.0	127	7	ADJ76886	Adj76886 Anti-IGF-
4	636	100.0	127	σ	ADZ67056	Adz67056 Murine im
S	569.5	89.5	118	7	ADJ76904	Adj76904 Anti-IGF-
y	569.5	89.5	118	Φ	ADZ67074	Adz67074 Mouse ant
7	550	86.5	118	~	AAW00829	Aaw00829 Variable
œ	550	86.5	118	~	AAW19015	Aaw19015 Anti-huma
σ	549	86.3	114	σ	AEA40137	Aea40137 TNF resis
10	548.5	86.2	118	7	ABR82776	Abr82776 Hybridoma
11	548.5	86.2	118	7	ABR82886	
12	546	85.8	117	7	ADJ76909	Adj76909 Anti-IGF-
13	546	85.8	117	σ	ADZ67079	Adz67079 Human ant
14	546	85.8	119	9	ABB98905	
15	546	85.8	135	7	ADJ76911	Adj76911 Anti-IGF-
16	546	85.8	135	σ	ADZ67081	Adz67081 Human ant
17	544.5	85.6	136	٣	AAY94391	Aay94391 Mouse VH
18	542	85.2	119	9	ABB98906	Abb98906 Variable
19	541.5	85.1	369	4	AAB73388	Aab73388 Anti-VHSV
20	541	85.1	117	7	ADB97814	4
21	541	85.1	117	7	ADJ76913	Adj76913 Anti-IGF-
22	541	85.1	117	σ	ADZ67083	m
23	541	85.1	135	7	ADJ76915	Adj76915 Anti-IGF-
24	541	85.1	135	9	ADZ67085	Adz67085 Human ant

25	539.5	84.9	119	2 5	AAW01584 ADG32325	Aaw01584 Lead bind Adq32325 Mouse BCF
27	539.5	84.8	371		ADG32362	
28	539.5	84.8	979	7	ADG32340	Adg32340 Fusion pr
29	538	84.6	522	0	AEC20775	
30	536	84.3	119	9	ABB98908	
31	533.5	83.9	119	σ	ADZ45405	Adz45405 Murine fa
32	533.5	83.9	468	σ	ADY91369	Ady91369 Anti-KID3
33	532	83.6	116	σ	ADZ45341	Adz45341 Murine fa
34	532	83.6	116	6	ADZ51254	Adz51254 Amino aci
35	532	83.6	116	6	ADZ42128	
36	531.5	83.6	118	8	ADT07572	Adt07572 Polypepti
37	531.5	83.6	243	æ	ADT07627	Adt07627 Polypepti
38	531.5	83.6	244	œ	ADT07628	Adt07628 Polypepti
39	529	83.2	117	7	ADJ76917	Adj76917 Anti-IGF-
40	529	83.2	117	σ	ADZ67087	Adz67087 Human ant
41	529	83.2	135	7	ADJ76919	Adj76919 Anti-IGF-
42	529	83.2	135	σ	ADZ67089	Adz67089 Human ant
43	527.5	82.9	116	œ	ADT89035	Adt89035 Murine pl
44	526	82.7	114	σ	AEA40153	Aea40153 Mouse Igh
45	524.5	82.5	118	σ	ADZ81874	Adz81874 Anti-lami

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these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; brasst tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipeoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 KPSLKDRISITRDTSKNQPFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
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                                                                                                                                                                                                                                                                                                                100.0%; Score 636; DB 7; 100.0%; Pred. No. 1.2e-51;
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20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
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                                                                                                                                                                                                                                                                                                                                                Similarity
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CORVAIA N.
LEGER O.
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                                                                                                                                                                                                                                                      Sequence 117 AA;
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                                                                                                                                                                                                                                                                                                                                                                             Matches 117;
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Best Local 8
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(HAEU/) I
(BECK/) I
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(LEGE/)
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AD2670
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Interpretation traders to a novel resoluted anti-insulinities growing to appale of the property (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of capable of binding tromaine kinase activity of the receptor.

C comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acida (ADZ67016). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a cartivation of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induced a connected with inhibition of the insulin creeptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent and/or EGF-dependent and/or a medicament intended for the specific targeting of a biologically active compound to a medicament intended for the specific
invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of IGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.
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100.0%; Pred. No. 1.2e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ76886 standard; protein; 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Matches 117; Conservative
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or epidermal growth factor receptor (IGFR) and/or with these receptors with their ligands. Especially they inhibit transformation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis, ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 52; 164pp; French
                                                                                                                                                                                                                                                                 (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                    18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
                                                                                                                                                                                                                                                                                                                                                     Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-569653/53.
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                                                                                                                                 KPSLKDRISITRDTSKNOPPLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                      KPSLKDRISITRDTSKNOFFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 127
                                                                                         DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                  Gaps
                                  ö
100.0%; Score 636; DB 7; Length 127; 100.0%; Pred. No. 1.3e-51; ive 0; Mismatches 0; Indels (
                 Local Similarity 100.
1es 117; Conservative
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   Query Match
                      Best Loca
Matches
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Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; heavy chain variable region.
                                                                                                                               Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:52.
                               ADZ67056 standard; protein; 127 AA
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                    Mus musculus.
                                                                                                30-JUN-2005
                  ADZ6705
RESULT
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Sequence 127 AA;

/note= "leader peptide" Location/Qualifiers

> Peptide Region

/note= "CDR1"

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The invertion relates to a novel isolated anti-insulinities growin factor of the invertion relates to a novel isolated anti-insulinities being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67001). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a cativation of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent and/or EGF-dependent cells, preferably IGF-dependent, cells connects of the cancer, of medicament intended for prevention or for the preparation of a medicament intended for prevention or for the preparation of a medicament intended for the specially get a biologically active compound to intended for the special for inversesing the IGF-IR and/or EGFR receptor. (I) is useful for inversesing or overexpressing of a biologically active compound or an underexpressing of a biologically act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leger O, Duflos A, Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 8; SEQ ID NO 52; 125pp; English.
61. .76
/note= "CDR2"
109. .116
/note= "CDR3"
                                                                                                                                                                                                                                                            18-JAN-2002; 2002FR-00000554.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                              16-DEC-2003; 2003US-00735916
                                                                                                                                                                                                                                         2002FR-00000653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-321968/33.
                                                                                                                                                                                                                                                                                                                                                                         GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                    DUFLOS A.
HAEUW J.
BECK A.
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                                                                                                            US2005084906-A1
                                                                                                                                                                                                                                         18-JAN-2002;
                                                                                                                                                   21-APR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (DUFL/)
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                                                                                                                                                                                                                                                                                                                                                                         (COET/)
    Region
                                                                                                                                                                                                                                                                                                                                                                                                                    (LEGE/
                                               Region
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Page

Gaps

1;

Indels

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Mismatches

5

Matches 107; Conservative

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (1) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or receptor (IGFR) and/or with of Signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit around transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and slow abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                 insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                        KPSLKDRISITRDISKNOFFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                    DVOLOESGPGLVKPSOSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                       DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                   Gaps
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   Length 127;
                                  Indels
; Score 636; DB 9;
; Pred. No. 1.3e-51;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 70; 164pp; French
                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                            ADJ76904 standard; protein; 118 AA
                                                                                                                                                                                                                                                                                                                                                                  Anti-IGF-1R related protein #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leger 0;
 100.0%;
100.0%;
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18-JAN-2002; 2002FR-00000654.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JAN-2003; 2003WO-FR000178
                                                                                                                                                                                                                                                                                                                                (first entry)
                                  Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goetsch L, Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-569653/53.
                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003059951-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                06-MAY-2004
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 Query Match
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Score 569.5; DB 7 Pred. No. 1.9e-45;

89.5%;

Query Match Best Local Similarity

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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyroshine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a madicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal hyperactivation of the IGF-IR and/or connected with a hyperactivation of the IR-IR and/or septiment mediated by the interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
                                                                                                                                                                                                                                                                                                                                                neoplasm; prostate tumor; andrology; genttourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                         61 NPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCAREGYGYFFDYWGQGTTLTVSS 118
                                                                 61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCARYG-RVFFDYWGQGTTLTVSS 117
                                  1 DVÓLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYINYDGNNNY
1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                     Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
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                                                                                                                                                                                                                                                                                                    Mouse antibody heavy chain variable region SEQ ID NO:70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 13; SEQ ID NO 70; 125pp; English.
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                                                                                                                                                                                            ADZ67074 standard; protein; 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JAN-2002; 2002FR-0000653.
18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-DEC-2003; 2003US-00735916
                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-321968/33.
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CORVAIA N.
LEGER O.
DUFLOS A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2005084906-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                  30-JUN-2005
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(HAEU/) I
(BECK/) I
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(LEGE/)
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                                                                                                                                                           RESULT 6
                                                                                                                                                                            ADZ67074
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the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral
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                                                                                                                                                                                              character, preferably IGP-dependent, especially IGP1 and/or IGF2—dependent and/or HER2/neu-dependent cells. (I) is useful for preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGP-dependent, and/or the proliferation of tumor cells, preferably IGP-dependent, especially IGP-and/or IGP2-dependent and/or EGP-dependent and/or EGP-dependent and/or HER2/neu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the prevention of a medic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cells expressing or overexpressing the IGF-IR and/or EGFR re
is useful for in vitro diagnosis of illnesses induced by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 118 AA;
     $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
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61 KPSLKDRISITRDISKNQFFLKLNSVTNEDTATYYCARYG-RVFFDYWGQGTTLTVSS 117 61 NPSLKNRISITRDISKNOFFLKINSVTTEDTATYYCAREGYGYFFDYWGQGTTLTVSS 118 1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY 1; Length 118; Indels DB 9; Score 569.5; DB 9; Pred. No. 1.9e-45; 2; Mismatches 8; 89.5**%**; 90.7**%**; Best Local Similarity 90.7 Matches 107; Conservative Query Match 8 셤 ð 셤

9 9

Gaps

Variable heavy chain of anti-human Fas ligand antibody NOK-4. AAW00829 standard; protein; 118 AA (first entry) 19-MAY-1997 AAW00829; AAW00829 RESULT 

Variable region; heavy chain; human; Fas ligand; monoclonal; antibody; NOK-4 hybridoma; inhibition; apoptosis; assay; diagnosis; disease; hepatitis; infectious mononucleosis; systemic lupus erythematosus.

Mus musculus

WO9629350-A1

26-SEP-1996

21-MAR-1996;

95JP-00087420 95JP-00303492 20-MAR-1995; 27-OCT-1995;

96WO-JP000734

(SUME ) SUMITOMO ELECTRIC IND CO.

Nakata Okumura K, Yagita H, Kayagaki N,

N-PSDB; AAT39555

WPI; 1996-443140/44.

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The present sequence is the heavy chain variable region of the anti-human Fas ligand monoclonal antibody (MAb) NOK-4. NOK-4 is produced by the hybridoma NOK-4 (FERM BP-5047), which was prepared by immunising mice with transformed human Ras ligand expressing COS cells, and fushing spleen cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CR1-1580) cells. The MAb recognises the human Fas ligand on the cell surface or in solution, and can be used to inhibit the apoptosis inducing cell surface Fas ligand/Fas reaction. The MAb can also be used for a Fas ligand assay in biological samples (e.g. human blood), especially for disease diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-human Fas Ligand antibody to treat hepatitis – controls apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                 2 VOLOESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK 61
                                                                                                                                                                                                                                                                                                                                                                                                      1 VQLQESGPGLVXFSQSLSLTCSVTGYSITSGYYWWIRQFPGNKLEWMGYISYDGSNNYN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSLKDRISITRDISKNOFFLKLNSVTNEDTATYYCA--RYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the heavy chain variable region of the murine anti-human Fas ligand (FasL) monoclonal antibody (MAD) NOK4, which is expressed by the hybridoma NOK4 (FERM BP-5044). The MAD can be used in the preparation of a composition for the effective oral or parenteral treatment of hepatitis, including hepatitis caused by hepatitis B or C virus. The composition controls apoptosis in liver cells caused by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heavy chain; variable region; mouse; murine; human; Fas ligand; FasL; monoclonal antibody; MAb; hybridoma; treatment; hepatitis; hepatitis B virus; HBV; hepatitis C virus; HCV; apoptosis; liver cell; glutamate oxaloacetate; pyruvate transaminase.
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                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-human Fast antibody (NOK4) heavy chain variable region.
                                                                                                                                                                                                                                                                                                      Score 550; DB 2; Length 118; Pred. No. 1.3e-43; 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakata M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Okumura K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              liver cells and improves liver function.
                25; Page 86-87; 133pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 36-37; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW19015 standard; protein; 118 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SUME ) SUMITOMO ELECTRIC IND CO.
                                                                                                                                                                                                                                                                                                          86.5%;
88.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-JP003089,
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                                                                                                                                                                                                                                                                                                                                             Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-258767/23.
                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                         Sequence 118 AA;
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                                                                                                                                                                                                                                                                                                             Query Match
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                  Claim
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Monoclonal antibody specifically recognising the Fas ligand - useful for the detection of Fas ligands either on cell surface or in solution.

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RESULT 10
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ID ABR8
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binding of FaeL to Fae expressing liver cells, and improves liver the function by improving blood glutamate oxaloacetate and pyruvate transaminase levels. The composition is given in a dosage of 0.0001-1000, preferably 0.01-600 mg/day. Spleen cells from mice immunised with FaeL expressing COS cells were fused with mouse myeloma cells to produce hybridomas. The hybridomas were screened for anti-FaeL activity, and the active clones NOKL-S isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for preparing variable region genes of high affinity tumor necrosis factor (TMF) resistant monoclonal antibody (F6 mAb). The method comprises using recombinant human TMF immune BALB/c mouse to prepare mouse anti-TMF monoclonal antibody, screening high
                                                                                                                                                                                        61
                                                                                                                                                                                                                 1 VOLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWWWIRQFPGNKLEWMGYISYDGSNNYN 60
                                                                                                                                                                                                                                                        PSLKDRISITRDISKNQFFLKLNSVTNEDTATYYCA -- RYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                       VOLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK
                                                                                                                                                              Gaps
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                                                                                                                                                              5,
                                                                                                                                                                                                                                                                                                                                                                                                                                           necrosis factor; TNF; monoclonal antibody; P6 mAb; chain variable region; heavy chain variable region; F6VH.
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                                                                                                                                    Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Variable region gene of high affinity monoclonal antibody necrosis factor and its preparation.
                                                                                                                     Score 550; DB 2; Lengtn LL. Pred. No. 1.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                   TNF resistant monoclonal antibody VH region, F6VH protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "CDR3"
/note= "Specifically claimed in Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Specifically claimed in Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "CDR2"
/note= "Specifically claimed in Claim
                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYFO-) UNIV FOURTH MILITARY MEDICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                   AEA40137 standard; protein; 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28. .33
/note= "CDR1"
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                                                                                                                                 Query Match
Best Local Similarity 88.1%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96. .103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2005-153078/17.
N-PSDB; AEA40136.
                                                                                                                                  Query Match
Best Local Similarity
                                                                                                          Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2005
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Region
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affinity F6 mAb using an indirect enzyme linked immunosorbent assay (ELISA). By cloning the monoclonal antibody light chain and heavy chain variable region (VL and VH respectively) genes, the monoclonal antibody light chain and heavy chain variable region gene sequence and amino acid sequence can be obtained, and the unicity of the gene sequence and protein sequence can be confirmed. This sequence represents the amino
                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD22; B-cell malignancy; anti-CD22 antibody; cytostatic; human; HB22-33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hybridoma HB22-33 anti-CD22 MAb heavy chain Vh-D-Jh junction sequence.
                                                                                                                                                                                                                                                                   LOESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYKPS
                                                                                                                                                                                                                                                                                                       1 LOESGPGLVKPSOSLSLTCSVSGYSITSGYFWNWIRQFSGNKLEWMGYISYDGSNNYNPS
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                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                              LKDRISITRDISKNOPPLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                  114
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                                                                                                                                                                                           Length 114;
                                                                                                                                                                                                                                8; Indels
                                                                                                                                                                                         Score 549; DB 9;
Pred. No. 1.5e-43;
5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 31; Fig 15; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR82776 standard; protein; 118
                                                                                                                                                                                           86.3%;
88.6%;
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                                                                                                                                                                                                                                Matches 101; Conservative
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(REGC ) UNIV CALIFORNIA.
                                                                                                                acid sequence for F6VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuscano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-712652/67.
                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ACF36426
                                                                                                                                                       Sequence 114 AA;
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ADJ76909;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to treating a human patient diagnosed with an autoimmune disease. The method involves administering to the patient an amount of a blocking anti-CD22 monoclonal antibody and monitoring the response of the autoimmune disease to the treatment. The method is useful in treating autoimmune disease (e.g. glomerulonephritis, systemic lupus erythematosus, rheumatoid arthritis, psoriasis, ulcerative colitis, Hashimoto's thyroiditis, autoimmune haemolytic anemias, diabetes or allergies) or B-cell malignancies (e.g. lymphomas or leukemias). The present sequence represents the amino acid sequence for heavy chain Vh-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating an autoimmune disease or a B-cell malignancy in a human patient comprises administering an amount of an anti-CD22 monoclonal antibody to the patient and monitoring the response of the disease to the treatment.
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                                                                                                                                             NPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCARGGITVAMDYWGQGTSVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                   CD22; autoimmune disease; anti-CD22 antibody; iImmunosuppressive; cytostatic; nephrotropic; dermatological; antiinflammatory; anti-ulcer; antirheumatic; antiarthritic; antipsoriatic; thyromimetic; antianemic; antidiabetic; antiallergic; gene therapy; HB22-33.
                                                                                                                           61 KPSLKDRISITRDISKNOPFLKLMSVTNEDTATYYCARYG-RVFFDYWGQGTTLTVSS 117
                                                                                   1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                 Gaps
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 Length 118;
                                                                                                                                                                                                                                                                                                                                        Hybridoma HB22-33 anti-CD22 MAb heavy chain (VH) fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence represents the amino acid sequence for hy
Jh junction for anti-CD22 antibody from hybridoma HB22-33
                               Indels
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Pred. No. 1.8e-43;
 Score 548.5; DB 7
Pred. No. 1.8e-43;
                              5; Mismatches
                                                                                                                                                                                                                                         $
                                                                                                                                                                                                                                        ABR82886 standard; protein; 118
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86.2%;
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2002US-0420472P.
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ilarity 87.3%;
Conservative
                                                                                                                                                                                                                                                                                                       (first entry)
                                 103; Conservative
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                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYDU-) UNIV DUKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ACF36494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-FEB-2002;
                                                                                                                                                                                                                                                                                                         18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-SEP-2003
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 Query Match
Best Local S
                                                                                                                                                                                                                                                                         ABR82886;
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine chinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or receptor (EGFR) and/or with chyperactivity of signal transduction pathways mediated by interaction of hyperactivity of signal transduction pathways mediated by interaction of transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                        61 NPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCARGGITVAMDYWGQGTSVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK
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61 KPSLKDRISITRDTSKNOFFLKLNSVTNEDTATYYCARYG-RVFFDYWGQGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 75; 164pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-IGF-1R related protein #22.
                                                                                                                                                                                                                                             ADJ76909 standard; protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
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                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-569653/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003059951-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
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Indels

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5; Mismatches

Best Local Similarity Matches 103; Conserv

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1 EVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYIRYDGSNNY

1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY

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PSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117

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The invention relates to a novel isolated anti-insulin-like growth factor

I receptor (IGF-IR) antibody (I) or its functional fragment, being
capable of binding to human IGF-IR and, if necessary, capable of
specifically inhibiting tyrosine kinase activity of the receptor,
comprising a light or heavy chain having at least one complementary
comprising a light or heavy chain having at least one complementary
comprising a light or heavy chain having at least one complementary
comprising a light or heavy chain having at least one complementary
comprising a light or heavy chain having at least one complementary
containing reggion (CDR) consisting of one of two fully defined 16 amino
activation of a medicament intended for the prevention or treatment
containing reggion (CDR) and/or EGRF, and/or connected with a
hyperactivation of the IGF-IR and/or of EGRF, where
the administration of the medicament does not induce or oily slightly
induces secondary effects connected with inhibition of the insulin
containing region of the medicament does not induce or oily slightly
contactor, The antibody is useful for preparation of a medicament intended
conhibit the transformation of normal cells into cells with tumoral
conhibit the transformation of normal edpendent cells with the growth
cueful for preparation of a medicament intended to inhibit the growth
and/or the proliferation of tumor cells, preferably IGF-dependent,
cueful for preparation of a medicament intended to inhibit the growth
                                                                                                                                                                                                                       neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                        Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
                                                                                                                                                              Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duflos A, Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; SEQ ID NO 75; 125pp; English.
                                      ADZ67079 standard; protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leger O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002FR-00000654.
2002FR-00005753.
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11-JUL-2003; 2003FR-00008538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for treating cancer.
                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-321968/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DUFLOS A. HAEUW J.
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                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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07-MAY-2002;
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                                                                                                                        30-JUN-2005
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                                                                                ADZ67079;
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(DUFL/)
(HAEU/)
(BECK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GOET/)
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RESULT 13
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             HERZ/neu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer of soleosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor at any in the suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene encoding anti-bisphenol A antibody, a recombinant protein and its preparation, a DNA, a vector, a transformant, preparation of a recombinant protein, a kit for determining bisphenol A.
                                                                                                                                                                                                                                                                                                                                                                                                                           2 VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to sequences for murine heavy chain variable region or light chain variable region of anti-bisphenol A antibody (ABZ21157-ABZ21164 and ABB98905-ABB98912). The sequences are useful for the preparation of recombinant protein
                                                                                                                                                                                                                                                                                                                                                                                                      2 VOLOBSGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 PSLKDRISITRDISKNOFFLKLNSVINEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Variable region; anti-bisphenol A; antibody; murine; heavy chain;
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                              Score 546; DB 9; Length 117; Pred. No. 3e-43;
                                                                                                                                                                                                                                                                                                                                                                    8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variable region anti-bisphenol A antibody chain #1.
                                                                                                                                                                                                                                                                                                                                                                  8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB98905 standard; protein; 119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 11; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOS-) BIO APPLIED SYSTEMS KK
                                                                                                                                                                                                                                                                                                                                85.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-096537/09.
N-PSDB; ABZ21157.
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                                                                                                                                                                                                                                                                                                                                                                      Matches 100;
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856666666666666666555X&
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85.8%; Score 546; DB 6; Length 119;

Query Match

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1 R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or prostate, lung, breast, endometrium and colon, also osteosarcoma, and prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                           9
                                                                                                                                                                                                                                           61 KPSLKDRISITRDTSKNQFFLKLASVTNEDTATYYCAR-YGRVF-FDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                    61 NPSLKORISITRDISKOQFFLKLNSVTPEDIATYYCARVLGRGYGLDYWGQGTSVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                          DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                     Gaps
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87.4%; Pred. No. 3.1e-43;
tive 5; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ76911 standard; protein; 135 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-IGP-1R related protein #23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2002; 2002FR-0000653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                         104; Conservative
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   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003059951-A2
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                                         Matches
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Gaps

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85.8%; Score 546; DB 7; Length 135; 86.2%; Pred. No. 3.5e-43; Live 8; Mismatches 8; Indels

Query Match
Best Local Similarity 86.2
Matches 100; Conservative

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PSLKDRISITRDTSKNOPFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                      80 PSLKORITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVPFDYWGQGTLVTVSS 135
                                                                                                                      Search completed: January 10, 2006, 20:44:16 Job time : 81.7649 secs
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       8
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OM protein - protein search, using sw model

January 10, 2006, 20:28:02; Search time 14.1157 Seconds (without alignments) 797.508 Million cell updates/sec Run on:

US-10-735-916A-69 636 1 DVQLQESGPGLVKPSQSLSL......RYGRVFFDYWGQGTTLTVSS 117 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	chain	eavy	Ig heavy chain V r	neavy	neavy	neavy	neavy	leavy	neavy	neavy	leavy	neavy	neavy chain	neavy	neavy	leavy	leavy	leavy	3 C72	neavy	Ig heavy chain V r	heavy	heavy	heavy		Ig variable region	mu chain	>	
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Score	545	535	523	521.5	521	519.5	510	508.5	504	503.5	503	503	499.5	499.5	499	476	470.5	463	462	461.5	457	455	447	425	423.5	423	422.5	420.5	413
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## ALIGNMENTS

4; Gaps Query Match 85.7%; Score 545; DB 2; Length 121; Best Local Similarity 86.0%; Pred. No. 5.3e-43; Matches 104; Conservative 3; Mismatches 10; Indels

1;

9 1 DVQLQESGPGLVKPSQSLSLFCSVTGYSITSSYYWNWIRQFPGNKLEWMGXISYDGRNDY 1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY 셤 ઠે

61 KPSLKDRISITRDTSKNOPPLKLNSVTNEDTATYYCARYGRV----FPDYWGQGTTLTVS 116 ð 셤

117 S 117 121 \$ 121 Š 셤

RESULT 2

Avm353

Avm354

Avm355

Avm355

Gradual precursor V region (MOPC 315) - mouse

Gradual Mus musculus (house mouse)

Gradual State (house mouse)

Gradual State (house mouse)

Gradual State (house mouse)

Gradual State (house mouse)

Rrainfret, A.; Horne, C.; Dorrington, K.J.; Klein, M.

Mol. Immunol. 26, 431-434, 1989

A;Title: Cloning, sequencing and expression of the rearranged MOPC 315 VH gene segment. A;Reference number: PL0102; MUD:89238351; PMID:2497341

A;Reference number: PL0102

A;Molecule type: mRNA

A;Residuas: 1-137 cRIN>

A;Coss-references: UNIPROT:P01822; UNIPARC:UP1000002727B; GB:M27638; NID:g602706; PIDN A;Represimental source: strain MOPC 315

R;Rinfret, A.; Dorrington, K.J.; Klein, M.

Skinfret, A.; Dorrington, K.J.; Klein, M.

submitted to the EMBL Data Library, June 1988

germ-lin

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A;Accession: E25114
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Residues: 1-119 <OLL)
A;Cross-terences: UNIPARC:UPI0000115D24; GB:X03378; NID:G52007; PIDN:CAA27095.1; PID:g.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPARC:UP10000117542; EMBL:X76018; NID:g416102; PIDN:CAA53605.1; PI C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin momology c! Keywords: heterotetramer; immunoglobulin homology c!MM>
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A; Residues: 1-117 cSHE>
A; Cross-references: UNIPARC: UP10000114D72; GB:M19775; NID:g195526; PIDN:AAA38343.1; PID
A; Note: the authors translated the codon AAC for residue 61 as Thr, and did not translat
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology < IMM>
F;15-98/Domain: immunoglobulin homology < IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C;Accession: 128195
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid the A;Reference number: A28195; MUID:88153717; PMID:3267217
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A,Title: The idiotypic network and the internal image: possible regulation of A,Reference number: A91028; MUID:86136012; PMID:3937730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38718
R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A;Accession: S38718
A;Accession: S38718
A;Accession: S38718
A;Status: preliminary
A;Aolecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NPSLKSRISITRDTSKNOPFLQLNSVTTEDTATYYCAR-GGTGFTFWGGGTLVTVSA 116
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C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
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Pred. No. 5.3e-41;
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83.8%; Pred. No. 7.1e-41;
cive 5; Mismatches 13
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Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 99; Conserv
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Affacession: A99914
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84.1%; Score 535; DB 1; Le
Best Local Similarity 83.2%; Pred. No. 5e-42;
Matches 99; Conservative 7; Mismatches 11;
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A;Molecule type: mRNA
A;Residues: 1-120 <OLL>
A;Cross-references: UNIPARC:UP10000115D15; GB:X03374; NID:g51983; PIDN:CAA27071.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hererotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region (HP12) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 20-Jun-2000
C;Accession: F22114
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
R;Ollier, P.; Rocca-Serra, A.; Somme, G.; Theze, J.; Fougereau, M.
A;Title: The idiotypic network and the internal image: possible regulation of a germ-lir A;Reference number: A91028; MUID:86136012; PMID:3937730
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C;Species: Mus musculus (house mouse)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jul-2000
C;Accession: A25114
R;Ollier, P:; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
B;Ollier, P:; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
B;Ditle: The idiotypic network and the internal image: possible regulation of A;Reference number: A91028; MUID:86136012; PMID:3937730
          1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
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Pred. No. 2.8e-39;
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Ig heavy chain precursor V region (40-140) - mouse
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81.7%; Pred. No. z.v.
5; Mismatches
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Matches 95; Conserv
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A; Residues: 1-115 <OLL>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: O7-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999
C;Accession: S07637
R;Urakov, D.N.; Deev, S.M.; Polyanovsky, O.L.
Nucleic Acids Res. 17, 9481, 1989
A;Tile: The structure of the expressible VH gene from a hybridoma producing monoclonal
A;Reference number: S07637; MUD:9067954; PMID:2587273
A;Molecule type: DNA
A;Residues: 1-136 <URA>
A;Residues: 1-136 <URA>
A;Residues: 1-136 <URA>
A;Cores-references: UNIPARC:UPI0000115E36; EMBL:X16740; NID:952099; PIDN:CAA34714.1; PIC
A;Note: the authors translated the codon TAT for residue 112 as 11e, TAC for residue 113
C;Genetics:
A;Note: the authors translated the codon TAT for residue 112 as 11e, TAC for residue 113
C;Genetics:
C;Genetics: Musunoglobulin N region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology <INM>
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C;Species: Mus musculus (house mouse)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C;Accession: C53285
R;Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 1063-1072, 1991
A;Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struct and their pH-reactivity profiles.
A;Reference number: A53285; MulD:92017897; PMID:1922102
A;Reference number: A53285; MulD:92017897; PMID:1922102
A;Accession: C53285
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C53285
Ig heavy chain V and J regions, monoclonal antibody OHP7D7.2.3 - mouse (fragment)
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                                                                                                                                                                                                                                                                                                                       NPSLKTRISITRDTSKNOFFLQLNSVTTEDTATYYCARDNGNCGDYWGQGTSVTVSS 117
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                    Length 117;
Score 521; DB 2; Lucas
Pred. No. 8e-41;
Tred. Indels
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Best Local Similarity 83.8%; Pred. No. 1.3e-40;
Matches 98; Conservative 6; Mismatches 12
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                 81.9%;
ilarity 83.8%;
Conservative
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Best Local Similarity
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C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PLO100
R;Near, R.I.; Haber, E.
Mol. Immunol. 26, 371-382, 1989
A;Title: Characterization of the heavy and light chain immunoglobulin variable region ge
A;Title: Characterization of the heavy and light chain immunoglobulin variable region ge
A;Title: Characterization of the heavy and light chain immunoglobulin variable region ge
A;Title: Characterization of the heavy and light chain immunoglobulin
A;Reference number: PLO100
A;Molecule type: DNA
A;Residues: 1-135 ~NEA>
A;Rossidues: 1-135 ~NEA>
A;Residues: 1-135 ~NEA>
A;Residues: 1-135 ~NEA>
A;Rossidues: 1-135 ~NEA>
A;Rossidues: 1-135 ~NEA>
A;Rossidues: 1-135 ~NEA>
A;Rossidues: 1-135 ~NEA>
A;Cross-references: UNIPARC:UPI000114EA6; GB:M27660; NID:g341745; PIDN:AAAS8746.1; PID:
A;Note: the VH40-140 gene segment is classified as a member of the 36-60 VH gene family
C;Genetics:
A;Introns: 15/1
C;Superfamily: immunoglobulin V region; immunoglobulin
P;1-18/Domain: signal sequence #status predicted <NEA>
F;11-118/Domain: immunoglobulin homology <IMC>
F;11-118/Domain: J segment #status predicted <NEA>
F;11-118/Domain: J segment #status predicted <NEA>
F;11-118/Domain: J segment #status predicted <NEA>
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Best Local Similarity
Matches 96; Conserva
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Ig heavy chain precursor V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999
C;Accession: 530752
R;Grant, P.J; Levin, S.D; Gilbert, T.; Kindsvogel, W.
Ricleic Acids Res. 15, 5496, 1987
A;Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.
A;Reference number: 530751
A;Accession: 530752
A;Accession: 530752
A;Accession: 530752
A;Accession: 530752
A;Residues: 1-149 cGRA-
A;Cross-references: UNIPARC:UPIO000115D92; EMBL:X05878; NID:g52526; PIDN:CAA29302.1; PID
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology < rMM>F;33-116/Domain: c region (C-gamma 2b) (fragment) #status predicted <CRE>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C;Accession: T01262
R;Pirofski, L.A.; Thomas, B.K.; Scharff, M.D.
A;DS Res. Hum. Retroviruses 9, 41-49, 1993
A;Title: Variable region gene utilization and mutation in a group of neutralizing murine A;Reference number: Z14285; MUID:93152285; PMID:7678971
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain precursor V region (VGAM3-2) - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Acess: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 18-Oct-1996 C;Acession: B24672 R;Winter, E.; Radbruch, A.; Krawinkel, U. BMBO.J. 4, 2861-2867, 1985 A;Reference number: A1022; MUID:86055722; PMID:2998759 A;Reference number: A1022; MUID:8605722; PMID:2998759 A;Reference number: A1022; PMID:2998759 A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 DVQLQESGPDLVXPSQSLSLTCTVTGYSITSGYTWHWIRQFPGNKLEWMAYIHYSGNTDF
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Pred. No. 7.2e-39;
6; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.1%; Score 503; DB 2;
79.8%; Pred. No. 4.6e-39;
tive 8; Mismatches 14;
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A;Molecule type: mRNA
A;Residues: 1-114 <PIR>
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Best Local Similarity 81.2%;
Matches 95; Conservative 6
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                        Gaps
A;Cross-references: UNIPARC:UPI00001768F5
A;Note: this sequence was determined from the differentiated gene
C;Genetics
C;Genetics
A;Introns: 15/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;19-134/Product: Ig heavy chain V region VGAM3-2 #status predicted <MAT>
F;33-116/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                        7;
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RESULT 15 HVMS31

Howay chain precursor V region (M315) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: JT0509
R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary in A;Reference number: JT050; MUID:89279149; PMID:2499654
A;Accession: JT0509
A;Accession: JT0509
A;Retures: translation not shown
A;Molecule type: mRNA
A;Residues: 1-116 <LEV>
A;Coss-references: UNIRROT:P18531; UNIPARC:UPI00000278E0
A;Coss-references: UNIRROT:P18531; UNIPARC:UPI00000278E0
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: lig heavy chain V region (M315) #status predicted <MAT>
F;19-116/Domain: signal sequence #status predicted <SIG>
F;33-116/Domain: immunoglobulin homology <IMM>

1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY Gaps ö 78.5%; Score 499; DB 1; Length 116; illarity 93.9%; Pred. No. 8.2e-39; Conservative 2; Mismatches 4; Indels Query Match Best Local Similarity Matches 92; Conserv

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99 NPSLKORISITRDTSKNQFFLKLNSVTTEDTATYYCAR 116

completed: January 10, 2006, 20:55:14 Search completed: Janua: Job time : 14.1157 secs

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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                2166443 segs, 705528306 residues
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651042 MOUSE
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                                                                                                                      January 10, 2006, 20:26:41;
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months old;

K. TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months old;

K. TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months old;

K. TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months 242603899;

K. Stauberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

K. Altschul S.F., Zeeberg B., Barder L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Both of the M.J., Garres M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu K., Gibbs R.A.,

Rahey J., Helton E., Kettemen M., Madan A., Rodriques S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Manderfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                      homo sapien
homo sapien
homo sapien
                                                                         rattus norv
homo sapien
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mus musculu
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homo sapien
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Bukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
P01819
O9u175
O9u175
O906331
O906331
O72374
O9072374
O904000
O6090000
O906330
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STRAIN-MIX FVB/N;
STRAIN-MIX FVB/N;
NIH MGC Project;
NIH MGC Project;
Submitteed (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002091; AAH02091.1; -; mRNA.
HSSP; PO1820; 1G7.1; -; mRNA.
HSSP; PO1820; 1G7.1; -; mRNA.
InterPro; IPR007110; 1g-1ike.
InterPro; IPR007110; 1g-1ike.
InterPro; IPR003006; 1g-MFC.
InterPro; IPR003596; 1g-V.
InterPro; IPR003596; 1g-V.
FRAM; PF07654; C1.eet; 2.
SWART; SM00406; 1Gv; 1.
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                   479 AA
                0901.75 HUMAN
HV21 HUMAN
096E70 - UUMAN
096E71 - HUMAN
06NY13 74 HUMAN
06NY13 - HUMAN
098UX14 HUMAN
096UX10 - HUMAN
096AX5 HUMAN
096AA6 - HUMAN
096AA6 - HUMAN
                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                          Q9BQB8 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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01-UTN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
LOCC38447 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                   Q99M22_MOUSE PRELIMINARY;
      1144
1122
1122
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STRAIN=Mix FVB/N;
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    MOUSE
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89238351; PubMed=2497341; DOI=10.1016/0161-5890(89)90133-8; Rinfret A., Horne C., Dorrington K.J., Klein M.; "Cloning, sequencing and expression of the rearranged MOPC 315 VH gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN SEQUENCE OF 19-136.

MEDLINE=74170779; PubMed=4524622;

Francis S.H., Leelie R.G.Q., Hood L., Eisen H.N.;

Manino-acid sequence of the variable region of the heavy (alpha) chain of a mouse myeloma protein with anti-hapten activity.";

Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
                                                                                                                                                                      61 KPSLKDRISITRDTSKNOFFLKLANSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                   79 NPSLKNRISITRDTSKNOFFLKLNSVTTEDTATYYCASRGYSWFPNWGQGTLVTVSA 135
                                                                                                                               DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQPPGNKLEWMGYINYDGSNNY
                                                                                                                  1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLMNWIRQFPGNKLEWMGYISYDGTNNY
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                        Gaps
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MEDLINE=79148758; PubMed=428562;
Schechter I., Wolff O., Zemell R., Burstein Y.;
"Structure and function of immunoglobulin genes and precursors.";
Fed. Proc. 38:1839-1845(1979).
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Hood L., Margolies M.N., Givol D., Zakut R.;
Unpublished results, cited by:
Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
-!- MISCELLANEOUS: This alpha chain was isolated from a myeloma protein that has anti-dinitrophenyl activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jilka R.L., Pestka S.; "Amino acid sequence of the precursor region of MOPC-315 mouse
                                                                Length 479;
                                                            Match 85.1%; Score 541; DB 2; Length 47 Local Similarity 85.5%; Pred. No. 1.7e-47; Local 100; Conservative 6; Mismatches 11; Indels
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Immunoglobulin domain.
SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin heavy chain.";
Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977)
                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
01-AJG-1992 (Rel. 23, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10 heavy chain V region MOPC 315 precursor.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                             137 AA
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MEDLINE=78094475; Pubmed=414225;
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                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                            HV46 MOUSE
P01822;
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                                                               Query Match
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klauener R.D., Collins F., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                      heavy chain V region MOPC 315.
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G -> GG (in Ref. 1; CAA30727).

G -> H (in Ref. 2).

GY -> YG (in Ref. 4).

N -> D (in Ref. 4).

Missing (in Ref. 4).
                                                                                                                                                                                                                                                                                                                                 Complementarity-determining-1.
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Framework-3.
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Framework-4.
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Last annotation update)
                                                                                                                                                                                                                  Immunoglobulin domain;
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Pred. No. 1.6e-47;
7; Mismatches 11;
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Genomic_DNA
Genomic_DNA
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Framework-1
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                                                                                                                        InterPro; IPR00310; Ig-like.
InterPro; IPR003596; Ig-v.
SWART; SM00406; IGv; 1.
Divect protein sequencing; Immunog.
                                                             HSSP; P01820; 1G7J.
SMR; P01822; 20-137.
Ensembl; ENSMUSG0000057048; Mus
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EMBL; M27638; AAA61337.1; -; EMBL; X07880; CAA30727.1; -;
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QSU413;
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                                                                                                                                                                                                                                                                                                           PL0102; AVMS35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
NUCLEOTIDE SEQUENCE.
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Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLECTIDE SEQUENCE.
MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 DVQLQESGPDLVKPSQSLSLTCTVTGYSITSGYGWHWIRQFPGNKLEWMGYISYSGSNNY
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                                                                           NIH MGC Project;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC085312; AAH85312.1; -; mENA.
Ensembl; ENSMUSG00000054328; Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                     SMAAL) SWESTER | 16 LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SROUENCE 483 AA; 52714 MW; 7C272DAS01A4A0D1 CRC64;
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                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 526.5; DB 2;
Pred. No. 5.4e-46;
7; Mismatches 11;
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                                                                                                                                                                                                                                                            GO; GO:0003823; F:antigen binding; IEA
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig.MHC.
InterPro; IPR003596; Ig.v.
Pfam; PP07654; Cl-set; Z.
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llarity 82.5%;
Conservative
                                                                                                                                                             NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N; TISSUE=Colon;
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                                                                                                              and mouse cDNA sequences."
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Q53VQ5;
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SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
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hes 99; Conserv
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Submitted (N
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MEDLINE=90067954; PubMed=2587273;

A Urakov D.N., Deev S.M., Polyanovsky O.L.;

The structure of the expressible VH gene from a hybridoma producing monoclonal antibodies against porcine transferrin.";

INUCLEIC Acids Res. 17:9481-9481(1989).

INUCLEIC Acids Res. 17:9481-9481(1989).

REBL; X16740; CAA34714.1; -; Genomic_DNA.

RISSP; P18832; 1KCV.

R RKSP; P18832; 1KCV.

R RRP; QCLBG5; 20-136.

R InterPro; IPR003599; IG.

R InterPro; IPR003599; IG.

R InterPro; IPR00404; IG.

R SMART; SM00409; IG.1.

R SMART; SM00406; IG.Y.

R RRSSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                             VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLMNWIRQFPGNKLEWMGYISYDGTNNYK 61
                                                                                                                           61 KPSLKDRISITRDISKNOPFLKLNSVTNEDTATYYCA----RYGRVFF---DYWGQGT 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 VOLQESGPGLVKPSQSLSLTCSVTDFSITSGYYWHWIRQFPGNKLEWMGYISYDGSNGYN
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                    1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYISYDGSHNY
                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
oglires; Glires; Rodentia; Sciurognathi;
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Indels
Score 523; DB 2; Length 11 Pred. No. 2.5e-46; 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 136 AA; 15307 MW; 5B0F439CCFB15C3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q53VR7 MOUSE PRELIMINARY; PRT; 120 AA.
Q53VR7;
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
VH-D-UH region (Fragment).
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 519.5; DB 2;
Pred. No. 6.7e-46;
6; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata
Mammalia, Eutheria, Euarchontoglires,
                                                                                                                                                                                                                                                                           Created)
   82.2%;
83.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.7%;
83.8%;
                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, VH gene product (Fragment).
                                                                                                                                                                                                                                           QELBQS MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98; Conservative
                                 99; Conservative
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                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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NUCLEOTIDE SEQUENCE
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                   Similarity
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   Query Match
Best Local S:
Matches 99
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                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                          MEDLINE=86136012; PubMed=3937730; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system."; EMBO J. 4:3681-3688(1985).
          Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; "The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
                                                                                                                                                                                                                                                            1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                          DVHLOESGEGETVXPSQSLSLTCSVTCYSITRGYNWNWIRRFFGUKLEWMGYINYDGSNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCARYG----RVFFDYWGQGT 111
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د
                                                                                                                                                                                                      80.0%; Score 508.5; DB 2; Length 120; 79.2%; Pred. No. 8e-45; ive 8; Mismatches 8; Indels 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Indels
                                                                                                              Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03375; CAA27077.1; -; mRNA.
EMBL; X03374; CAA27071.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases EMBL; X03379; CAA27101.1; -; mRNA.
                                                                                                                                                                                13892 MW; 013452306EBAA3BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D465A5854DF459A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 31, Last sequence update) (TrEMBLrel. 31, Last annotation update)
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81.7%; Pred. No. 2.2e-44;
ive 5; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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MEDLINE=86136012; PubMed=3937730;
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                                                                                       NUCLEOTIDE SEQUENCE OF 28-29.
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                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VH-D-JH region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                   Q53VQ1_MOUSE PRELIMINARY;
Q53VQ1:
                                                             EMBO J. 4:3681-3688(1985)
                                                                                                                                                                                                                     Local Similarity 79.2
ses 95; Conservative
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                                                                                                                                                                                120 AA;
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Submitted (NOV
                                                                                                      Fougereau M.;
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13-SEP-2005
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCAR--PLYFRHDEEYYDVMDYWGQG 118
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Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during the
                                                                                                                                                                                                                                                                            NUCLECTIDE SEQUENCE.
MEDILINE=86136012; PubMed=3937730;
MEDILINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
The idiotypic network and the internal image: possible regulation of a germ-line network by pauchgene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
EMBO J. 4:3681-3688(1985).
                                                                                                                                             Mammalia; Eutheria; Unordata; Craniata; Vertebrata; Euteleostomi; Muridae; Murinae; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DVQLQESGPGLVKPSQSLSLTCSVTGNSITSGYYWSWIRQFPGNKLEWMGYIKYDGNNSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.1%; Score 503; DB 2; Length 119; 79.3%; Pred. No. 3e-44; tive 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03376; CAA27083.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 119 119 119 119 AW; 36504D1665BFBB59 CRC64;
                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
IIG heavy chain V region M315 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 AA
PRT;
                                               Created)
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J. Exp. Med. 169:2007-2019(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE OF 28-29.
                                             13-SEP-2005 (TIEMBLED. 31, 13-SEP-2005 (TIEMBLED. 31, 13-SEP-2005 (TIEMBLED. 31,
                                                                                                                VH-D-JH region (Fragment).
QS3VR3 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96; Conservative
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                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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NUCLEOTIDE SEQUENCE.
TISSUE=Spleen;
NIH MGC Project;
Submitted (APR-2005)
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MEDLINE-2218825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MA Klausher R.D., Felngold E.A., Grouse L.H., Derge J.G.,
MA Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Malstechenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Nablas S.D., Loquellano N.B., Dorando M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Raheto J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Gimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Generation and initial analysis of more than 15,000 full-length human
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                    Ensembl; ENSMUSGO000057048; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IRR003596; Ig-v.
SMART; SMO0406; IGv. 1.
BROSTIR; PS50835; IG LIKE; 1.
3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.5%; Score 499; DB 1; Length 116; 93.9%; Pred. No. 7.5e-44;
                                                                                                                                                                                                                                                                                        Complementarity-determining-1
                                                                                                                                                                                                                                                                                                                                      Complementarity-determining-2
                                                                                                                                                                                                                                              chain V region M315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 NPSLKNRISITRDTSKNQPFLKLNSVTTEDTATYYCAR 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 590 AA
                                                                                                                                                                                                                                                                                                                                                                                   By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muroidea; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                           PDB; 1EZV; X-ray; X=22-116.
SMR; P18531; 19-116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similar to Igh-6 protein.
Name=LOC299357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q569B8_RAT PRELIMINARY;
Q569B8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                         JT0509; HVMS31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse
                                                                                                                                                                                                                                                                                                                                                                                                        NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                            CHAIN
REGION
REGION
                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                   REGION
                                                                                                                                                                                                                                                                                                                                      REGION
                                                                                                                                                                                                                                                                                                                                                               REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KPSLKDRISITRDISKNQFFLKLNSVTNEDTATYYCARYGRVF--FDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLECTIDE SEQUENCE.
MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYISYDGSHNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.

Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.

RMBL; BC092580; AAH92580.1; -; mRNA.

GO; GO:0003823; F:antigen binding; IEA.

A InterPro; IPR003199; Ig.

InterPro; IPR003199; Ig.

InterPro; IPR0031899; Ig.

InterPro; IPR003106; Ig.MHC.

RIMER PRO03106; Ig.MHC.

RASHAT; SM00409; IG.1.

RASHAT; SM00409; IG.1.

RESEQUENCE 590 AA; 65088 MW; FAC77FFA82302304 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               Score 492; DB 2; Length 590;
Pred. No. 2.6e-42;
7; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03378; CAA27096.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 AA; 11202 MW; 4049CF8C7EE8AAE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NPSLKNRISITRDTSKNQFFLKLNSVTIEDTATYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.2%; Score 491; DB 2; 92.9%; Pred. No. 4.2e-43; iive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                       77.4%;
79.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE OF 28-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q53VQ4 MOUSE PRELIMINARY;
Q53VQ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VH region (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Klausner R.D., Collins F.S., Wagner L.H., Berge J.G.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Baher N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Baher N.K.,
W. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hisher F.,
Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toophiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan R.J., Malan S.J., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,
W. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Hale S., García S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Rodriguez A.C., Grimwood S.J.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 NPSLKSRISITRDISKNQFFLQLNSVTTEDTATYYCARCHGGPLTGR-YFDYWGQGVMVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCAR-----YGRVFFDYWGQGTTLT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 EVQLQESGPGLVKPSQSLSLTCSVTGYSITSNY-WGWIRKFPGNKMEWIGHISYSGSTSY
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DVOLOESGPGLVKPSOSLSLTCSVTGYSITGGYLWNWIROFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.9%; Score 489; DB 2; Length 61
76.4%; Pred. No. 5.7e-42;
ive 10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC092582; AAH92582.1; -; mRNA.
GO; GO:0003823; F:antigen binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSS0835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; UNKNOWN 3.
SEQUENCE 615 AA; 67986 MW; BE5C2483C69F186C CRC64;
                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                615 AA
                                                                                                                                                                  Created)
                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INCEPPIO: 14M01559; 19.
INTERPO: 1PR007110; 19.
INTERPO: 1PR003597; 19_C1.
INTERPO: 1PR003006; 19_MHC.
INTERPO: 1PR003596; 19_V.
Pfam; PF07654; C1-8et; 4.
SMART; SM00407; 1G21; 4.
SMART; SM00407; 1G21; 4.
                                                                                                                                                        10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.'
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                                                                                         Q569B6_RAT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                               LOC314509 protein.
Name=LOC314509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Spleen;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 VSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Spleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94;
                           RESULT 12
Q569B6_RAT
                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DVHLQESGPGLVKPSQSLSLTCSVTGYSITRGYNWNWIRRFPGNKLEWMGYINYDGSNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=86136012; PubMed=3937730; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system."; EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.5%; Score 480; DB 2; Length 98; 88.8%; Pred. No. 5.8e-42; ive 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fougereau M.; Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases. EMBL; X03375; CAA27078.1; -; mRNA. EMBL; X03374; CAA27072.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 AA; 11255 MW; EBC71AA2F8F5FD60 CRC64;
                                                                                                                                            13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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Q53VQ9
13-SEP-2005 (TEMBLrel. 31,
13-SEP-2005 (TEMBLrel. 31,
13-SEP-2005 (TEMBLrel. 31,
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                                                                                                      Q53VR6_MOUSE PRELIMINARY;
Q53VR6;
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                                                                                                                                                                                                              VH-region (Fragment).
Mus musculus (Mouse).
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NUCLEOTIDE SEQUENCE.
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137 VSS 139
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NON TER
SEQUENCE
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0537R2 MOUSE PRELIMINARY; PRT; 98 AA.
0537R2 MOUSE (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
VH region (Fragment).
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLECTIDE SEQUENCE.
MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
"The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                        DVQLQESGPGLVKPSQSLSLTCSVTGYSIASGYYWSWFRQFPGDKLEWMGYISFDGNINY
                                                                                                                                8; Gaps
                                                                                          ch 74.8%; Score 476; DB 2; Length 119; 1 Similarity 75.4%; Pred. No. 1.9e-41; 89; Conservative 9; Mismatches 12; Indels
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EMBL; X03377; CAA27089.1; -; mRNA.
NON TER 1 1 1
NON TER 119 119
SEQÜENCE 119 AA; 13844 MW; 6B1
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                                                                                                             Best Local Similarity
Matches 89; Conserv
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Q53VR2 MOUSE
DQ53VR2 MC
AC Q53VR2 MT
DT 13-SEP-20
DT 13-SEP-20
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Search completed: January 10, 2006, 20:53:26 Job time : 79.8731 secs

1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLMNWIRQFPGNKLEWMGYISYDGTNNY

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RESULT 1
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_FUB.pep:*
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7: /cgn2_6/ptodata/1/pubpaa/US0_NEW_FUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US10_NEW_FUB.pep:*
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(c) 1993 - 2006 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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ALIGNMENTS

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SI ES		2-353	2-353-	2-353-	2-35	9-310-	-31	-31	-31	2-35	2-35	2-35	5-83	9-26	2-35	2-35	9-26	5-94	2-33	9-26	2-33	2-33	2-33	2-334	2-33	2-33
SUMMARIES		-012	-012	-012	-11-012	10-959	-10-959-310-3	10-959-310-3	-959 - 310 - 3	-01	11-012-353-4	-01	-12	-08	-01	-01	US-11-089-266-2	US-11-065-943	US-10-932-334-6	-08	-93	US-10-932-3	10-932-334	US-10-932	US-10-932-3	-93
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Length 112; Indels

100.0%; Score 595; DB 7; 100.0%; Pred. No. 2.8e-40; tive 0; Mismatches 0;

Query Match 100. Best Local Similarity 100. Matches 112; Conservative

; SOFTWARE: Patentin Ver. 3 ; SEQ ID NO 65 ; LENGTH: 112 ; TYPE: PRT ; ORGANISM: Homo sapiens US-11-012-353-65

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Sequence 86, Appl Sequence 90, Appl Sequence 65, Appl Sequence 30, Appl	Sequence 67, Appl Sequence 66, Appl Sequence 48, Appl Sequence 60, Appl Sequence 10, Appl	111, 59, 84, 85,	Sequence 8, Appl Sequence 58, Appl Sequence 62, Appl Sequence 82, Appl Sequence 50, Appl Sequence 58, Appl
	US-10-512-184-67 US-10-512-184-66 US-10-512-184-48 US-10-932-334-10 US-10-932-334-10	US-10-932-334-11 US-10-932-334-59 US-10-932-334-84 US-10-932-334-85 US-10-932-334-94	US-10-932-334-8 US-10-932-334-58 US-10-932-334-62 US-10-932-334-82 US-11-932-334-50 US-11-012-353-58
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KESULI 1 US-11-012-353-65
; Sequence 65, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
, APPLICANT: GOETSCH, LILLIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
, TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
, TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patentin Ver. 3.3

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US-11-012-353-63
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                                                                                                                                                                                                                                 TYPE: PRT
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TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: US/35,916
PRIOR PILING DATE: 2003-12-16
PRIOR PILING DATE: 2003-07-11
PRIOR PLILING DATE: 2002-01-20
PRIOR PLILING DATE: 2002-01-20
PRIOR PLILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-01-18
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APPLICANT: LEGER, OLIVIER
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND SES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR FILING DATE: 2004-12-16
PRIOR PLICATION NUMBER: PR
PRIOR PLICATION NUMBER: PR
PRIOR PLILING DATE: 2003-07-11
PRIOR PLILING DATE: 2003-07-11
PRIOR PLILING DATE: 2003-01-20
PRIOR PLILING DATE: 2003-01-20
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PRIOR PLILING DATE: 2003-01-20
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Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
                           Sequence 67, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
                                                                                                                                                        APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
BAPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
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Best Local Similarity 100.0
Matches 112; Conservative
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ORGANISM: Homo sapiens
-11-012-353-67
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US-11-012-353-61
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TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 01773-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: RR 0308538
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2003-07-07
PRIOR FILING DATE: 2002-01-20
PRIOR FILING DATE: 2002-01-20
PRIOR FILING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 594; DB 7; Length 112;
Pred. No. 3.4e-40;
1; Mismatches 0; Indels
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOOTWARE: Patentin Ver. 3.3
SEQ ID NO 61
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 63, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GORTSCH, LILLANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.1%;
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-012-353-61
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61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSLLPWTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: Synthetic peptide
                                                                                                     Sequence 34, Application US/10959310; Publication No. US20050287138A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 35
LENGTH: 112
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US-10-959-310-35
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Pred. No. 1.7e-36;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 112;
                                                                      Sequence 25. Application US/10959310
Publication No. US2000287138A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KYOWA HAKCO KOGYO CO., LTD.
TITLE OF INVENTION: CCR4 specific antibody composition
FILE REFERENCE: 249-363
CURRENT FILING DATE: 2004-10-07
PRIOR FILING DATE: 2003-10-08
PRIOR PLING DATE: 2003-10-08
PRIOR PLING DATE: 2004-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 112
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; Sequence 33, Application US/10959310
; Publication No. US20050287138A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OP INVENTION: CCR4-specific antibody composition
; TITLE REPRENCE: 249-363
; CURRENT APPLICATION NUMBER: US/10/959,310
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: US 60/572,784
; PRIOR PILING DATE: 2003-10-08
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 33
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
91.9%; Score 547; DB 6;
Best Local Similarity 92.0%; Pred. No. 1.4e-36;
Matches 103; Conservative 5; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Synthetic peptide US-10-959-310-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic peptide US-10-959-310-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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Best Local Similarity 91.1%;
Matches 102; Conservative
                                                                    US-10-959-310-26
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1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60 1 DILMIQSPLSLPVIPGEPASISCRSSRNIVHINGDTYLEWYLQKPGQSPQLLIYKVSNRF 60 1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL Gaps 61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112 ö Query Match 91.4%; Score 544; DB 6; Length 112; Best Local Similarity 91.1%; Pred. No. 2.5e-36; Matches 102; Conservative 6; Mismatches 4; Indels Query Match
91.3%; Score 543; DB 6; Length 112;
Best Local Similarity 90.2%; Pred. No. 2.9e-36;
Matches 101; Conservative 7; Mismatches 4; Indels Sequence 35, Application US/10959310
Publication No. US20050287138A1
GENERAL INFORMATION:
TITLE OF INVENTION: CCR4-specific antibody composition
FILE REPRESENCE: 249-363
CURRENT APPLICATION NUMBER: US/10/959,310
CURRENT APPLICATION NUMBER: US 2003-15062
FRIOR FILING DATE: 2003-10-08
FRIOR APPLICATION NUMBER: US 60/572,784
FRIOR FILING DATE: 2004-05-21 TITLE OF INVENTION CCR4-specific antibody composition TITLE OF INVENTION: CCR4-specific antibody composition; FILE REFERENCE: 249-363 and CURRENT APPLICATION NUMBER: US/10/959,310 CURRENT FILING DATE: 2004-10-07; PRIOR APPLICATION NUMBER: US 60/572,784 prior APPLICATION OF SEQ 1D NOS: 46

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TYPE: PRT
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Best Local (
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                                                                                                                                                                                                         Sequence 54, Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HAGUW, JEAN-FRANCOIS
APPLICANT: HAGUW, NEEFFORE ANTI-IGF-IR AND/OR ANTI-INSULIN/IGP-I HYBRID
TITLE OF INVENTION: NOTESTER SAITH SETTION NOTESTER TO 17753-199
CURRENT FILING DATE: 2004-12-16
FRIOR FILING DATE: 2003-12-16
FRIOR FILING DATE: 2003-07-11
FRIOR PELLOR NUMBER: FR 0308538
FRIOR FILING DATE: 2003-07-11
FRIOR FILING DATE: 2003-07-11
FRIOR FILING DATE: 2003-07-11
FRIOR FILING DATE: 2003-07-11
FRIOR FILING DATE: 2002-01-08
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2003-01-18
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Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GORTSCH, LILIANE

APPLICANT: GORTSCH, LILIANE

APPLICANT: DUFLOS, ALAIN

APPLICANT: BECK, ALAIN

APPLICANT: BECK, ALAIN

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION NUMBER: US/11/012,353

CURRENT PILING DATE: 2004-12-16

PRIOR APPLICATION NUMBER: FR 0308538

PRIOR FILING DATE: 2003-07-11
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61 SGVPDRPSGSGSGTDFTLKISRVEAEDVGVYYCFQGSLLPWTFGQGTKVEIK 112
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; ORGANISM: Mus musculus
US-11-012-353-54
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US-11-012-353-49
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### TRICR APPLICATION NUMBER: PCT_PR03/00178
### PRICR APPLICATION NUMBER: PC 200573
### PRICR APPLICATION NUMBER: PR 200573
### PRICR APPLICATION NUMBER: PR 200573
### PRICR APPLICATION NUMBER: PR 200503
### PRICR PLINE DATE: 2002-01-80 200504
### PRICR PLINE DATE: 2002-01-80 20054
### PRICR PLINE DATE: 2002-01-80 20054
### PRICR PLINE DATE: 2003-01-80 20055
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Query Match
Best Local Similarity 85.7%
Matches 96; Conservative
APPLICATION NUMBER:
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; Sequence 66, Application US20050287148A1
; GENERAL INFORMATION:
    APPLICANT: Chatterjee, Malaya
    APPLICANT: Chatterjee, Sunil K.
    TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA NUMBER OF SEQUENCES: 6
    CORRESPONDENCE ADDRESS:
    ADDRESSER: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD
    CITY: PALO ALTO
    STRATE: CA
    COUNTRY: USA
    ZIP: 94304-1018
    COMPUTER: IBM PC compatible
    COMPUTER: IBM PC compatible
    COMPUTER: IBM PC compatible
    COMPUTER: Patentin Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/11/089,266
    FILING BATE: 23-Mar-2005
    CLASSIFICATION:
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                                61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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                                                                                                                                                      Sequence 23, Application US/11125837
Publication No. US20050266003A1
GENERAL INFORMATION:
APPLICANT: Lin, Rong-Hwa
APPLICANT: Chang, Chung Nan
APPLICANT: Chen, Pel-Jun
APPLICANT: Chen, Pel-Jun
APPLICANT: Hang, Chiu-Chen
TITLE OF INVENTION: ANTIBODIES
FILE REFRERENCE: 1306-2-011001
CURRENT APPLICATION NUMBER: US/11/125,837
CURRENT APPLICATION NUMBER: US 60/569,892
PRIOR APPLICATION NUMBER: US 60/569,892
PRIOR APPLICATION NUMBER: US 60/569,892
NUMBER OF SEQ ID NOS: 100
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
SEQ ID NO 23
TYPE: PRT
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APPLICATION NUMBER: US/10/153,401
FILING DATE: 27-Aug-2002
APPLICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mus musculus US-11-125-837-23
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Sequence S5, Application US/11012353
; Bouldation No. US20050249730A1
; GENERAL INFORMATION:
APPLICANT: OGETSCH. LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
FILE REFERENCE: 017753-196
FRIOR REILING DATE: 2003-12-16
FRIOR APPLICATION NUMBER: PR 0308538
FRIOR FILING DATE: 2003-07-11
FRIOR FILING DATE: 2003-07-11
FRIOR PELING DATE: 2003-07-11
FRIOR PELING DATE: 2002-05-07
FRIOR APPLICATION NUMBER: FR 020653
FRIOR PELING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 521; DB 7; Length 263;
Pred. No. 3e-34;
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85.7%; Pred. No. 2.1e-34;
tive 11; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.6%; Scc...
86.6%; Pred. No. .c.
'''a 8; Mismatches
PILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
FILING DATE: 1996-01-16
ATTORNEY/AGENT INFORMATION:
NAME: Catherine M. Polizzi
REGISTRATION NUMBER: 40,130
RESTERENCE/DOCKET NUMBER: 304142000202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPRONE: (415) 813-5600
TELEPRONE: (415) 813-5600
TELERA: 706141
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
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SOFTWARE: PatentIn Ver. 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 86.6
Matches 97; Conservative
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RESULT 15

US-11-012-353-57

i Sequence 57, Application US/11012353

j Publication No. US20050249730A1

j GENERAL INFORMATION:

j APPLICANT: GOSTSH, LILIANE

j APPLICANT: GOSTSH, LILIANE

j APPLICANT: HEGREY, DEATHNIE

j APPLICANT: BECK, ALAIN

j APPLICANT: BECK, ALAIN

j TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

j TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

j TITLE OF INVENTION: NUMBER: 10/735,916

prior PRIOR PILING DATE: 2004-12-16

prior PRIOR PILING DATE: 2003-12-16

prior PRIOR PILING DATE: 2003-12-16

prior PRIOR PILING DATE: 2003-07-11

prior APPLICATION NUMBER: FR 020553

prior APPLICATION NUMBER: FR 020553

prior APPLICATION NUMBER: FR 020553

prior APPLICATION NUMBER: FR 0200554

prior PRIOR PILING DATE: 2002-05-07

prior PRIOR PILING DATE: 2002-05-07

prior APPLICATION NUMBER: FR 0200554

prior APPLICATION NUMBER: PR 0200554

prior APPLI
                                                    DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-57
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 Query Match
 87.2%; Score 519; DB 7; Length 112;

 Best Local Similarity 85.7%; Pred. No. 2.1e-34;
 6. Conservative 11; Mismatches 5; Indels 0; Gaps 0;

 Matches 96; Conservative 11; Mismatches 5; Indels 0; Gaps 0;
 0;

 Qy
 1 DIVWTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQWPGQSPQLLIYKVSNRL 60

 Db
 1 DVVWTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 60

Search completed: January 10, 2006, 21:36:23 Job time : 5.71144 secs

Sequence Seq

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Run on:

Sequence:

Database

Result No.

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DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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Sequence 65, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:
Mathalie

APPLICANT: GORYGAL, Liliane

APPLICANT: GORYGAL, Mathalie

APPLICANT: EEGER, Olivier

APPLICANT: BECK, Alain

APPLICANT: HEGER, Olivier

FILE REFERENCE: 01753-183

CURRENT FILING DATE: 2003-12-16

PRIOR APPLICATION NUMBER: PR 03/08 538

PRIOR PILING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: PR 02/00 653

PRIOR PILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-02-07

NUMBER OF SEQ ID NOS: 156
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100.0%; Pred. No. 1.5e-46;
tive 0; Mismatches 0;
US-10-505-980-19
US-10-500-207A-45
US-10-500-207A-43
US-10-231-452-13
US-10-505-980-20
US-09-753-436-66
US-10-163-942-66
US-10-745-115-66
US-10-434-469-21
US-10-434-469-21
US-10-434-469-21
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US-10-434-469-21
US-10-735-916A-54
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Best Local Similarity 100.
Matches 112; Conservative
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LENGTH: 112
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192, App
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107, App
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                                                                                                                                                                  ; Search time 61.4328 Seconds (without alignments) 761.757 Million cell updates/sec
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1 DIVWIQSPLSLPVIPGEPAS......CFQGSHVPWIFGQGTKVEIK 112
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cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US03_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                                version 5.1.6
- 2006 Compugen Ltd.
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US-10-735-916A-67
US-10-735-916A-63
US-10-433-698-1182
US-10-443-69-19
US-10-434-469-19
US-10-308-207A-19
US-10-500-207A-19
US-10-258-728-26
US-10-258-728-27
US-10-482-105-39
US-10-482-105-39
US-10-482-180
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US-10-483-698-181
US-10-453-698-181
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                                                                                                                                                                                                                                                                                                                                                                                                                                1867569 segs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length: 0
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Maximum DB
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Gaps

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Length 112; Indels

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99.8%;
99.1%;
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Best Local Similarity 99.1<sup>†</sup>
Matches 111; Conservative
                                                                Query Match
Best Local Similarity 99.1
Matches 111; Conservative
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US-10-735-916A-63
US-10-735-916A-61
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SEQ ID NO 63
LENGTH: 131
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GENERAL INFORMATION:
APPLICANT: GORTSCH, Liliane
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: DUFLOS, Alain
APPLICANT: BECR, Alain
APPLICANT: BECK, Alain
APPLICANT: MALW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: PR 03/08
FRIOR FILING DATE: 2003-07-11
FRIOR PELING DATE: 2003-07-11
FRIOR PELING DATE: 2003-01-20
FRIOR PELING DATE: 2002-01-18
FRIOR PELING DATE: 2002-05-07
FRIOR PELING DATE: 2002-05-07
FRIOR PELING DATE: 2002-05-07
FRIOR PELING DATE: 2002-05-07
FRIOR PELING DATE: 2002-01-18
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                                                                APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: DEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: HECK, Alain
TILLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
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Best Local Similarity 100.0%; Pred. No. 1.8e-46;
Matches 112; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                         FILE KEFEKENCE: 01/733-183

CURRENT PEDLICATION NUMBER: US/10/735,916A

CURRENT FILING DATE: 2003-12-16

PRIOR PELING DATE: 2003-07-11

PRIOR PILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-01-20

PRIOR PILING DATE: 2003-01-18

PRIOR FILING DATE: 2003-01-18

PRIOR APPLICATION NUMBER: FR 02/00 653

PRIOR APPLICATION NUMBER: FR 02/00 654

PRIOR APPLICATION NUMBER: FR 02/05

PRIOR PILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 156

SEQUENARE: PATENTIN VET. 2.1
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                                     APPLICANT: GOETSCH, Liliane
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CORGANISM: Homo sapiens
US-10-735-916A-67
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ORGANISM: Homo sapiens
GENERAL INFORMATION:
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US-10-735-916A-61
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Publication No. US20050084906A1

GENERAL INFORMATION:
APPLICANT: GOETSCH, Liliane
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
APPLICANT: APPLICATION NUMBER: FR 03/00 178
APPLOR FILING DATE: 2002-01-18
                                                                                                                                                                                                                                                                                                                 61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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Length 112;
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Score 594; DB 5;
Pred. No. 1.9e-46;
1; Mismatches 0
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Pred. No. 2.2e-46;
1; Mismatches 0
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APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
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RESULT 9
US-10-500-207A-19
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TITLE OF INVENTION: Anti-fiblroblast growth factor-8 monoclonal antibod
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                                                                                                                                         Query Match 94.8%; Score 564; DB 4; Length 112; Best Local Similarity 94.6%; Pred. No. 1e-43; Matches 106; Conservative 3; Mismatches 3; Indels
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TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 02 CIP (1087-37 CIP)
CURRENT APPLICATION NUMBER: US/10/453,698
CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Petentin version 3.2
LENGTH: 112
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PRIOR APPLICATION NUMBER: JP 08-081754
PRIOR PILING DATE: 1996-04-03
PRIOR APPLICATION NUMBER: US 08/832,236
PRIOR FILING DATE: 1997-04-03
PRIOR FILING DATE: 1997-06-07
PRIOR FILING DATE: 1999-06-07
PRIOR APPLICATION NUMBER: US 09/326,590
PRIOR APPLICATION NUMBER: US 09/876,040
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CURRENT APPLICATION NUMBER: US/10/434,469
CURRENT FILING DATE: 2003-05-09
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Publication No. US20040038308A1
GENERAL INFORMATION:
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Publication No. US20040091480A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1 SEQ ID NO 182 LENGTH: 112 TYPE: PRT
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Matches 106; Conservative
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Akiko FURUYA
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Kenya SHITARA
Naoki SHIMADA
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; ORGANISM: human
US-10-453-698-182
                                                                              ; ORGANISM: human
US-10-308-817-182
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US-10-434-469-19
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APPLICANT:
APPLICANT:
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APPLICANT: KYOWA HAKKO KOGYO CO., LTD
TITLE OF INVENTION: Humanized anti-FGF-8 antibody and the antibody fragment thereof
FILE REFERENCE: 11399W01
CURRENT APPLICATION NUMBER: US/10/482,105
CURRENT FILING DATE: 2003-12-24
PRIOR FPLING DATE: 2001-196176
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 41
SSOFTWARE: Patentin Ver. 2.1
SSQ ID NO 17
                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: VL synthetic peptide US-10-434-469-19
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Pred. No. 1e-43;
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Publication No. US20050175608A1
GENERAL INFORMATION:
APPLICANT: KYOWA HAKKO KOGYO CO., LTD
TITLE OF INVENTION: AGENT FOR TREATING ARTHRITIS
FILE REFERENCE: 1442
CURRENT APPLICATION NUMBER: US/10/500,207A
CURRENT APPLICATION NUMBER: US/2001-400677
PRIOR APPLICATION NUMBER: JOS001-400677
PRIOR FILING DATE: 2001-12-28
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                              Score 564; DB 4;
Pred. No. 1e-43;
4; Mismatches
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Best Local Similarity 94.6%;
Matches 106; Conservative
                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 112
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Best Local Similarity 94.61
Matches 106; Conservative
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; OTHER INFORMATION 108-10-500-2078-47
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LENGTH: 112
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APPLICANT: Blis, John Robert Maxwell
APPLICANT: Blis, John Robert Maxwell
APPLICANT: Durrant, Linda Gillian
FILE OF INVENTION: Humanised Antibodies to the Epidermal Growth Factor Receptor FILE REPERENCE: 28438-1010501
CURRENT APPLICATION NUMBER: US/10/258,728
CURRENT FILING DATE: 2003-06-18
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3:1
LENGTH: 112
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APPLICANT: KYOWA HAKKO KOGYO CO., LTD
TILLE OF INVENTION: AGENT FOR TREATING ARTHRITIS
FILE REFERENCE: 1442
CURRENT APPLICATION NUMBER: US/10/500,207A
CURRENT FILING DATE: 2004-66-28
FRICA APPLICATION NUMBER: JP2001-400677
PRIOR FILING DATE: 2001-12-28
NUMBER OF SEQ ID NOS: 51
SOFTWARE PALENTI Version 3.1
SEQ ID NO 47
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94.5%; Score 562; DB 4;
Best Local Similarity 92.9%; Pred. No. 1.5e-43;
Matches 104; Conservative 4; Mismatches 4.
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                                           TYPE: PRT ORGANISM: Artificial Sequence
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US-10-258-728-28
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                      LENGTH: 112
SEQ ID NO 19
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APPLICANT: Blis, John Robert Maxwell
APPLICANT: Blish, John Robert Maxwell
APPLICANT: Durrant, Linda Gillian
TITLE OF INVENTION: Humanised Antibodies to the Epidermal Growth Factor Receptor FILE REFERENCE: 28438-1010591.
CURRENT APPLICATION NUMBER: US/10/258,728
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: GB 0011981.8
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APPLICANT: Basi, Guriq
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
CURRENT APPLICANTION NUMBER: US,10/388,214A
CURRENT FILING DATE: 2003-03-12
PRIOR PILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 38
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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                                                                                                                                                                                      Length 112;
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Pred. No. 2.9e-43;
6; Mismatches 2;
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92.9%;
ORGANISM: Artificial Sequence
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Matches 104; Conservative
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US-10-258-728-26

Sequence 26, Application US/10258728

Sequence 26, Application Would Wou
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Pred. No. 4.4e-43;
4; Mismatches 5; Indels
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TITLE OF INVENTION: AGENT FOR TREATING ARTHRITIS
FILE REFERENCE: 1442
CURRENT APPLICATION NUMBER: US/10/500,207A
CURRENT PILING DATE: 2004-06-28
PRIOR APPLICATION NUMBER: JP2001-400677
PRIOR PILING DATE: 2001-12-28
NUMBER OF SEQ ID NOS: 51
                                                                                                                                                                                                                                                                                                                                                                                                      Score 558; DB 4;
Pred. No. 3.5e-43;
4; Mismatches 5
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: GB 0020794.4
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 27
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; Sequence 46, Application US/10500207A
; Publication No. US20050175608A1
; GENERAL INFORMATION:
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Best Local Similarity 92.0%;
Matches 103; Conservative
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ORGANISM: Mus musculus
US-10-258-728-26
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ORGANISM: Mus musculus
US-10-258-728-27
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Best Local Similarity
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RESULT 1
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Sequence
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.: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

:: /cgn2_6/ptodata/1/iaa/f_COMB.pep:*

:: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

:: /cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*

:: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

:: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-331-398A-50

US-08-331-3978-50

US-08-227-693-50

US-08-053-171-15

US-08-053-171-15

US-08-482-882-66

US-08-487-1399-66

US-08-487-1399-66

US-08-487-1399-66

US-08-487-1399-66

US-08-473-503-66

US-08-473-503-66

US-08-473-503-66

US-08-473-9308-95

US-08-134-346A-50

US-08-134-346A-50

US-08-175-680-66

US-08-175-680-66

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US-08-175-680-95

US-08-175-8388-95

US-08-175-888-95

US-08-176-3498-88
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US-08-077-252B-3
US-08-331-397B-48
US-08-759-804A-48
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S-08-752-844-66
S-09-293-533-66
                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                       572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              OM protein - protein search, using sw model
                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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595
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Match Length DB
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Perfect score:
                                                                                                                                                                    Scoring table:
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Maximum DB
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                                                                                                                                             Sequence:
                                                                                                                                                                                                       Searched:
                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
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Sequence 3, Appli Sequence 48, Appli Sequence 3, Appli Sequence 67, Appli Sequence 67, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 34, Appli Sequence 19, Appli	Sequence 29, Appl
US-09-002-753A-3 US-09-227-693-48 US-09-527-693-48 US-09-657-274-3 US-09-531-396N-67 US-08-331-3978-67 US-08-331-3978-66 US-08-759-844-2 US-08-759-844-2 US-08-591-396-2 US-09-293-533-2 US-09-293-533-2 US-08-311-3978-34 US-08-313-3978-34 US-08-313-3978-34 US-08-313-3978-34 US-08-313-3978-34 US-08-313-3978-34 US-08-313-3978-34 US-08-313-3978-34 US-08-313-3978-34	US-08-207-861-29
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Query Match
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Specific Antibody Fragments, Fusion Proteins, and Uses
Thereof
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                                                                                                                                                                                                                    1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                        61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPWTFGQGTKVBIK 112
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                                                                                                                                 Length 112;
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chain (V-L) (HumB3V-L)"
                                            /note= "Humanized B3 Variable Light
chain (V-L) (HumB3V-L)"
                                                                                                                             Query Match 93.9%; Score 559; DB 1; Length 11: Best Local Similarity 93.8%; Pred. No. 2.6e-47; Matches 105; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  015280-126120US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
PRIOR DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/767,331
PRIOR DATE: 10-SEP-1990
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 50, Application US/08331397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mut
TITLE OF INVENTION: Specific Antibod
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: HURLER, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
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COTHER INFORMATION:

CS-08-331-397B-50
h NAME/KEY: Protein LOCATION: 1..112
OTHER INFORMATION:
OTHER INFORMATION:
US-08-331-398A-50
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1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                     Gaps
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                                                                                                                                                                                                                              61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPFTFGQGTKVBIK 112
                                                     ö
Score 559; DB 1; Length 112;
Pred. No. 2.6e-47;
4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                        US-08-759-804A-50

Sequence 50, Application US/08759804A

Sequence 50, Application US/08759804A

Patent No. 5990296

GENERAL INFORMATION:
APPLICANT: PitzGerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Pusion Proteins, and Uses Thereof
NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Humanized B3 Variable Light
chain (V-L) (HumB3V-L)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
FILING DATE: 30-SEP-1991
FILING DATE: 12-OCT-1990
ATTOMENYAGEN: 110-OCT-1990
ATTOMENYAGEN: 110-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  015280-126140US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFRENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEPRA: (415) 576-0200
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
     93.9%;
                           Best Local Similarity 93.8
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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CTHER INFORMATION:
CTHER INFORMATION:
US-08-759-804A-50
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/note= "Residue that has been
replaced with mouse amino acid in the humanized
                                                                                                                            61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                             61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPFTFGQGTKVEIK 112
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region"
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region"
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                                                                                                                                                                                                                                                                                                              US-08-053-171-15
; Sequence 15, Application US/08053171
; Patent No. 5562903
; Patent LINCORMATION:
    APPLICANT: Co, Loibner:
    TITLE OF INVENTION: Antibody Derivatives
; TUMBER OF SEQUENCES: 32
; CORRESPONDERES: ADDRESS:
    ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER FRADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: TEM PC compatible

COPERATIOS SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/053,171

FILING DATE: 22-APR-1993

CLLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Smith, Willaim M

REGISTRATION NUMBER: 11823-54-1

TELEPRATION NUMBER: 1326-2400

TELEPRATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 112 amino acids

TYPE: amino acids

TYPE: AND COMPUTED COMPUTED
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LOCATION: 94..102
OTHER INFORMATION: /note=
OTHER INFORMATION: region'
FRATURE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEATURE:
NAME/KEY: REGION
LOCATION: 24.39
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: REGION
LOCATION: 55.61
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
Patent No. 5562903
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 54
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94301
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                                                                             1 DIVWIQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                      APPLICANT: BASTAN, Iraa
APPLICANT: BASTAN, Itaa
APPLICANT: BASTAN, Eduardo A.
APPLICANT: DEBNHAK, Itaai
APPLICANT: DADLAN, Eduardo A.
APPLICANT: JUNG, Sun-Hee
APPLICANT: LEE, Byungkook
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                 0; Gaps
                                                                                                                                                                                                                          61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                           61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPFTFGGGTKVEIK 112
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Best Local Similarity 93.8%; Pred. No. 2.6e-47; Matches 105; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: 1..112
; OTHER INFORMATION: /note= "Humanized B3 VL region"
US-09-227-693-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-126-1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9600
TELEPRAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acide
TYPE: amino acide
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
RECOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,396
FILING DATE:
RELOR APPLICATION DATA:
APPLICATION NUMBER: 07/767,331
FILING DATE: 30-SEE-1991
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50, Application US/09227693
Patent No. 6287562
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                         1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                                                                                                                             Gaps
                                                                                       /note= "Residue in the framework that is replaced with mouse amino acid in the humanized antibody."
                                                                                                                                                                                                                                                                                                                                                                                                                              61 SCVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPFTFGQGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                     61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVBIK 112
                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                            93.6%; Score 557; DB 1; Length 112; 94.6%; Pred. No. 4.1e-47; ive 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08815190A
Patent No. 6046310
GENERAL INFORMATION:
APPLICANT: Oueen, Cary L.
APPLICANT: Schneider, William P.
APPLICANT: Vaequez, Maximilian P.
TITLE OF INVENTION: Uses Ligand Fusion Proteins and Their
TITLE OF INVENTION: Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,190A
PILING DATE: 11-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,584
FILING DATE: 13-MAR-1996
ATTONEY/AGENT INPOMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 17
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TORNEY/AGENT INCOMENTAL Apple, Randolph T.
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPRENCE DOCKET NUMBER: 0118;
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYRE: amino acids
TYRE: amino acids
TYRE: amino acids
OTHER INFORMATION: antibody." FEATURE: NAME/KEY: Modified-site
                                                                                                                                                                                                                                       Best Local Simitairy
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MOLECULE TYPE: peptide
                                                                 LOCATION: 108
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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; OTHER INFORMATION:

US-08-815-190A-14
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                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-815-190A-14
                                                                                                                                                              US-08-053-171-15
                                                                                                                                                                                                               Query Match
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                                                                                                          1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                      0; Gaps
                                                                                                                                                                                                               61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                          61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPFTFGQGTKLEIK 112
Score 557; DB 2; Length 112;
Pred. No. 4.1e-47;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 544; DB 1; Length 116; Pred. No. 7.8e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                  US-08-482-882-66; Application US/08482882; Sequence 66, Application US/08482882; Sequence 66, Application US/08482882; Sequence 66, Application: STATE CENERAL INFORMATION: APPLICANT: Gallatin, W. Michael APPLICANT: Vazeux, Rosemay; TITLE OF INVENTION: ICAM-Related Materials and Methods; NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:

OPERATING SYSTEM:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,882

FILING DATE: 07-JUN-1995

CLASSIFCATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,754

FILING DATE: 08/102,852

FILING DATE: 08-AUG-1993

PRIOR APPLICATION NUMBER: US 08/009,266

FILING DATE: 20-AUG-1993

PRIOR APPLICATION NUMBER: US 08/009,266

FILING DATE: 20-AUN-1993

PRIOR APPLICATION NUMBER: US 07/894,061

FILING DATE: 12-AUN-1993

PRIOR APPLICATION NUMBER: US 07/894,061

FILING DATE: 15-AUN-1992

PRIOR APPLICATION NUMBER: US 07/889,724

FILING DATE: 26-ANN-1992

PRIOR APPLICATION NUMBER: US 07/889,724

FILING DATE: 26-ANN-1992

PRIOR APPLICATION NUMBER: US 07/889,724

FILING DATE: 18-ANN-1992

PRIOR APPLICATION NUMBER: US 07/827,689

FILING DATE: 17-ANN-1992

APPLICATION NUMBER: 37-302

REGISTRATION NUMBER: 35-302

REGISTRATION NUMBER: 35-302

REGISTRATION NUMBER: 35-302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 32178
TELECOMOTUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEFAX: 6-3666
INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.4%;
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amino acid
Query Match
Best Local Similarity 94.6
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-882-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 CCTY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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5 DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQXPGQSPQLLIYKVSNRF 64
                                                                        61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                         65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPYTFGQGTKVEIK 116
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL GALIBATIN, W. Michael
APPLICANT:
APPLICANT:
FITLE OF INVENTION:
INGRESSE:
ADBRESSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.4%; Score 544; DB 1; Length 116; 92.0%; Pred. No. 7.8e-46; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 08/286,754
PILING DATE: 05-AUG-1994
PRIOR APPLICATION NUMBER: US 08/102,852
PRIOR APPLICATION NUMBER: US 08/009,265
FILING DATE: 05-AUG-1993
PRIOR APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRICATION NUMBER: US 07/894,061
PILING DATE: 05-JUN-1992
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRICR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATPONNEY/AGENT INFORMATION:
NAME: NO. 5837822and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                 US-08-487-113D-66; Sequence 66, Application US/08487113D; Patent No. 5837822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 32744
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 116 amino acids TYPE: amino acid
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Best Local Similarity 92.04
Matches 103; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-487-113D-66
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                                                                                                             5 DIVMIQSPLSLPVIPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLIYKVSNRF 64
                                                                            1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
          0; Gaps
                                                                                                                                                                                                                   61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                       65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPYTFGQGTKVEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66, Application US/08483389

Sequence 66, Application US/08483389

Patent No. 581517

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay

TITLE OF INVENTION: ICAM-RELATED PROTEIN
NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive/6300 Sears Tower

CITY: Chicago
STATE: Illinois
COUNTRY: Onited States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 91.4%; Score 544; DB 1; Length 116; Best Local Similarity 92.0%; Pred. No. 7.8e-46; Matches 103; Conservative 4; Mismatches 5; Indels
       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America.

ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,389
FILING DATE: 0'-JUN-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 0'-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,724
FILING DATE: 2'-JAN-1992
PRIOR APPLICATION NUMBER: US 0'/899,724
FILING DATE: 2'-JAN-1992
PRIOR APPLICATION NUMBER: US 0'/899,724
FILING DATE: 2'-JAN-1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: P-41,337
REFERENCE/DOCKET NUMBER: 2'7-866/32760
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
TELEPHONICATION NUMBER: 2'-4048
TELERA: (312) 474-6448
TELERA: (312) 474-6448
TELERA: (312) 474-6448
TELERA: (312) 474-6300
TELEPHONICATION NUMBER: CANDAMATION:
TELEPHONE (CHARACTERISTICS:
LENGTH: 116 amino acids
TTYPE: AMINORARIAN ACIDS
TELEPHONE CHARACTERISTICS:
LENGTH: 116 amino acids
          4; Mismatches
          Matches 103; Conservative
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MOLECULE TYPE: protein
US-08-483-389-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                            61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: 1llinois COUNTRY: USA ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 544; DB 1; Length 11
Pred. No. 7.8e-46;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:

OPERATING SYSTEM:

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/08/473,503

FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

PRICK APPLICATION NUMBER: US/28,754

FILING DATE: 05-AUG-1994

APPLICATION NUMBER: US 08/102,852

FILING DATE: 05-AUG-1993

PRICK APPLICATION NUMBER: US 08/102,852

FILING DATE: 05-AUG-1993

PRICK APPLICATION NUMBER: US 08/009,266

FILING DATE: 25-JAN-1993

PRICK APPLICATION NUMBER: US 07/894,061

FILING DATE: 25-JAN-1993

PRICK APPLICATION NUMBER: US 07/894,061

FILING DATE: SS-JAN-1992

PRICK APPLICATION NUMBER: US 07/899,724

FILING DATE: SS-JAN-1992

PRILING DATE: SS-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 32178 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                    Sequence 66, Application US/08473503 Patent No. 5869262
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TELEFAX: (312) 474-0448
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Best Local Similarity 92.0%;
Matches 103; Conservative
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear; MOLECULE TYPE: protein US-08-473-503-66
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1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                              US-08-483-932-66; Application US/08483932
; Sequence 66, Application US/08483932
; Patent No. 5880268
; GENERAL INFORMATION:
    APPLICANT: Gallatin, W. Michael
    CORRESPONDENCES: 116
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
    STREET: 6300 Sears Tower, 233 S. Wacker Drive
    CITY: Chicago
    STATE: Illinois
    COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/483,932
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIPATEMENTS: 505 AGE
PRICK APPLICATION IDATA:
APPLICATION NUMBER: 08/286,754
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-OAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-UN-1992
PRIOR APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5880266and, Greta E.
REFERENCE/DOCKET NUMBER: 35.302
REFERENCE/DOCKET NUMBER: 35.3178
TELECOMMINICATION INFORMATION:
NAME: NO. 5880266and, Greta E.
REFERENCE/DOCKET NUMBER: 3178
TELECOMMINICATION INFORMATION:
THERECOMMINICATION INFORMATION:
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TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
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116 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                  US-08-714-017-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                   RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 1llinois COUNTRY: United States of America ZIP: 60606-6402 COMPUTRY READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OF COMPANION COMP
                                                                                                           VS-08-720-420A-66

Sequence 66, Application US/08720420A

Patent No. 5989843

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Vazeux, Rosemay

TITLE OP INVENTION: ICAM-Related Materials and Methods

NUMBER OF SEQUENCES: 120

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,420A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDER: US 08/487,113
FILING DATE: 05-70N-1995
FILING DATE: 05-805-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-805-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-0AN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-0AN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
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FILING DATE: 05-UN-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-UN-1992
ATTORNEY AGENT INFORMATION:
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REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
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INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
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amino acid
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Matches 103; Conservative
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1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 7.8e-46;
4; Mismatches 5; Indels
Sequence 66, Application US/08714017
Patent No. 6040176
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: JAZEUX, ROSEMBY
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PILING DATE:
PILING DATE:
PELLING DATE:
PELLING DATE:
PELLORATION NUMBER: US 08/102,852
PRIOR APPLICATION NUMBER: US 08/009,266
PILING DATE: 22-GAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-UN-1992
PRIOR APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6040176and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                        ZIP: 60606
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE:
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TELECOMMUNICATION INFORMATION:
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92.0%;
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TELEFAX: (312) 474-0448
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61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPWTFGQGTKVEIK 112

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5 DIVWIQSPLSLPVIPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRF 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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RESULT 14
US-08-475-680-66

Sequence 66, Application US/08475680

Sequence 67, Application US/08475680

Sequence 67, Application US/08475680

Setent No. 6100383

APPLICANT: Gallatin, W. Michael

APPLICANT: Vazeux, Rosemay

TITLE OF INVENTION: ICAM-Related Materials and Methods

NUMBER OF SEQUENCES: 116

CORRESPONDENCE ADDRESS:

ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: 111inois

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 116;
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Pred. No. 7.8e-46;
4; Mismatches 5; Indels
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COUNTRY:

COUNTRY:

COUNTRY:

COUNTRY:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Propay disk

MEDIUM TYPE: Propay disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAFFOLIN IR Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,680

FILING DATE: 05-AUG-1994

PRICH APPLICATION NUMBER: US/08/009,266

FILING DATE: 05-AUG-1993

PRICH APPLICATION NUMBER: US/08/009,266

FILING DATE: 20-JNN-1993

PRICH APPLICATION NUMBER: US/07/889,724

FILING DATE: 05-JUN-1992

PRICH APPLICATION NUMBER: US/07/889,724

FILING DATE: 26-MAY-1992

PRICH APPLICATION NUMBER: US/07/889,724

FILING DATE: 27-MAY-1992

PRICH APPLICATION NUMBER: US/07/889,724

PRICH APPLICATION UMMER: US/07/889,724

PRICH APPLICATION UMMER: 
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Best Local Similarity 92.0%;
Matches 103; Conservative
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1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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Sequence 95, Application US/08129930B
Fatent No. 5804187
GENERAL INFORMATION:
APPLICANT: Ceriani Dr., Fernando J.R.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Carcinoma Specificity, and Kit and TITLE OF INVENTION: Diagnostic Vaccination and TITLE OF INVENTION: Therapeutic Methods
TITLE OF INVENTION: Therapeutic Methods
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 91.3%; Score 543; DB 1; Length 131; Best Local Similarity 90.2%; Pred. No. 1.1e-45; Matches 101; Conservative 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SECTION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATTORNEY/AGRNT INFORMATION:
NAME: AMZEL PA. VÍVIDAB
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: CRFCC-008A
TELECROMMUNICATION INFORMATION:
TELERRAN: (510) 521-1333
TELERRAN: (510) 521-1333
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: V. AMZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 131 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Search completed: January 10, 2006, 20:58:03 Job time : 21.8706 secs

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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

January 10, 2006, 20:26:41 ; Search time 75.5025 Seconds (without alignments) 1046.577 Million cell updates/sec US-10-735-916A-65 595 1 DIVMIQSPLSLPVIPGEPAS......CFQGSHVPWIFGQGTKVEIK 112

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 Total number of hits satisfying chosen parameters:

2166443 segs, 705528306 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

1: uniprot_sprot:*
2: uniprot_trembl:* UniProt 05.80:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	a Bum	homo	рошо	0 homo		homo	mus	mus n	рошо	рошо	Q6pih6 homo sapien	рошо	-	_	P01615 homo sapien	_	рошо	Q5xkg4 mus musculu	mus	mus	EUM.	mus mu	P01618 canis famil	_	mus	mus m	homo	P18136 homo sapien	homot	homo	P01622 homo sapien
QI.	Q652Q7 9MURI	KV2E HUMAN	KV2F HUMAN	Q8NEKO HUMAN	KV2D HUMAN	Q9ULBO HUMAN	Q5F2I0_MOUSE	KV2G MOUSE	Q8TCD0 HUMAN	Q6P491_HUMAN	Q6PIH6 HUMAN	KV2A HUMAN	Q53VP8 MOUSE	Q652C0_MOUSE	KV2B HUMAN	Q58EU8_MOUSE	KV2C HUMAN	Q5XKG4 MOUSE	KV2F MOUSE	KV2E MOUSE	Q6LEM8 MOUSE	KV2D MOUSE	KV1 CANFA	KV4C HUMAN	KV2C_MOUSE	KV2A_MOUSE	KV4A_HUMAN	KV3M_HUMAN	KV4B_HUMAN	KV3B_HUMAN	KV3D_HUMAN
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& Query Match	87.2	83.9	83.9	83.7	82.0	81.4	81.3	81.0	80.7	80.5	79.6	79.2	79.2	78.5	76.3	75.6	75.5	74.1	72.9	72.3	70.4	6.69	67.0	8.99	65.0	64.7	63.4	63.4	62.2	61.8	61.8
Score	519	499	499	498	488	484.5	483.5	482	480	479	473.5	471.5	471	467	454	450	449.5	441	434	430	419	416	398.5	397.5	387	385	377.5	377	370	368	368
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P18135 homo sapien Q9ul78 homo sapien P01623 homo sapien	Q6kb05 mus musculu Q6kb05 mus musculu P01627 mus musculu P01619 homo sapien P04207 homo sapien	Q6pil8 homo sapien P01660 mus musculu P01624 homo sapien	Pole69 mus musculu Q52164 mus musculu
KV3L HUMAN Q9UL78 HUMAN KV3E HUMAN	NYSO MOUSE COKROOS MOUSE KV2B MOUSE KV3A HUMAN KV3H HUMAN	Q6PILB HUMAN KV3H MÕUSB KV3F HUMAN	KV3Q_MOUSE Q52L64_MOUSE
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129	120 120 108 108	236 111 109	111 240
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368 363 361	360.5 360.5 359 357 356	355.5 354.5 354	353.5 353.5
333	2 W W W W W W W W W W W W W W W W W W W	444	4 4 4 4 4 5

ALIGNMENTS

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                                                                                                                         1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQMYLQKPGQSPQLLIYKVSNRL
                                                                                  Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                             'Match B7.2%; Score 519; DB 2; Length 248; Local Similarity 86.6%; Pred. No. 6.1e-46; Local Similarity 9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-07N-1988 (Rel. 06, Created)
01-07N-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
11G kappa chain V-II region GM607 precursor (Fragment).
Homo sapiens (Human).
       055207

065207;

065207;

25-007-2004 (TrEMBLrel. 28, Created)

25-007-2004 (TrEMBLrel. 28, Last sequence update)

25-007-2004 (TrEMBLrel. 28, Last annotation update)

25-007-2004 (TrEMBLrel. 28, Last annotation update)

B3 (FV) - PE40 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P06309;
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KV2E HUMAN
065207
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REGION
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RAHAH
BORN DON
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                                                                                                                                                                                                                                                                                                                                        This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Complementarity-determining-3.
Framework-4.
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Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12664 MW; 92C57DC719E558B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z00009; -; NOT_ANNOTATED_CDS; Genomic_DNA. PIR; A01889; KZHUGM.
HSSP; Q99M37; 1191.
SMR; P060309; 5-117.
GO; GO:0005576; C:extracellular region; NAS. GO; GO:0005557; P:immune response; NAS. InterPro; IPR00319; P:immune response; NAS. InterPro; IPR00310; GO:1000555; P:immune response; NAS. InterPro; IPR00310; IQ-1ike.
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Pred. No. 3.1e-44;
2; Mismatches 13
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01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
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                                                                                                                                        NUCLEOTIDE SEQUENCE.
MEDLINE=84191506; PubMed=6325927;
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MEDLINE=86041852; PubMed=2997711;
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Matches 97; Conservative
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6410.
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.; "Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YGVPDRFSGSGGTDFTLKISRVBAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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Pred. No. 3.7e-44;
9; Mismatches 9; Indels
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PIR; A01890; KZHURP.

HISSP; Q99M37; 1191.

SMR; Po6310; Z1-133.

Ensembl; ENSG0000173758; Homo sapiens.

GO; GO:0005576; C:extracellular region; NAS.

GO; GO:0005576; P:amtigen binding; NAS.

HICEPPO; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

InterPro; IRR03356; IG LIKE; 1.

FROSITE; PS50835; IG LIKE; 1.
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villaton D.K., Murny D.M., Sodergran B.J., Lu X., Gibbs R.A., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Alesseley R.W., Touchman J. W., Green B.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human T. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            W. Klein R., Jaenichen R., Zachau H.G.;

KI Klein R., Jaenichen R., Zachau H.G.;

KI Klein R., Jaenichen R., Zachau H.G.;

L. Eur. J. Immunol. 23:3248-3262(1993).

R. Expressed human immunoglobulin kappa genes and their hypermutation.";

R. Embl. BC030814; AAH30814.1; -; mRNA.

R. FIR; S34091; S34091.

R. FIR; S40342; S40342.

R. FIR; S40357; S40357.

R. SSP; PO1834; 1172.

R. RSP; PO1834; 1172.

R. RSP; QREKC); 21-237.

R. RICEPPCO; IPRO03506; Ig_MHC.

R. InterPro; IPRO03596; Ig_V.

R. FEm.; PF07654; C1-set; 1.

DR. FEm.; PF07654; C1-set; 1.

DR. FMART; SM00406; IG_MHC; UNKNONN_1.
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                                                                                                                                                                                                                                                                               Huber C., Klobeck H.G., Zachau H.G.;
"Ongoing V kappa-J kappa recombination after formation of a productive
V kappa-J kappa coding joint."; V kappa Eur.
Bur. J. Immunol. 22:1561-1565(1992).
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"V kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the V kappa locus and do not show
somatic mutation.";
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 239 Aa; 26024 MW; F5E20AD3B0552COA CRC64;
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84.8%; Pred. No. 9.3e-44;
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                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last amnotation update)
1g kappa chain V-II region TEW.
1d kappa chain Wall region TEW.
Elwaryota, Menazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Glenner G.G.;
"Structural identity of Bence Jones and amyloid fibril proteins in a patient with plasma cell dyscrasia and amyloidosis.";
J. Ciln. Invest. 52:1276-1281(1973).
-!- MISCELLANBOUS: The major amyloid protein appears to be identical with the Bence Jones protein isolated from the same patient.
-!- MISCELLANBOUS: This protein was isolated from the urine of a patient with plasma cell dyscrasia and amyloidosis.
-!- MISCELLANBOUS: The C region of this chain has the INV (1,2)
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MEDLINE=74148480; PubMed=4596149;
Putnam F.W., Whitley B.J. Jr., Paul C., Davidson J.N.;
Manino acid sequence of a kappa Bence Jones protein from a case primary amyloidosis.";
Biochemistry 12:3763-3780(1973).
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R HSSP; Q99M7; 1191.
R SWR; PO1617; 1-1191.
R GO; GO:0005576; C:extracellular region; NAS.
R GO; GO:0005823; F:antigen binding; NAS.
R GO; GO:0006955; P:immune response; NAS.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003596; Ig-v.
R SWART; SW00406; IGV;
R ROSITE; PS50835; IG_LIKE; 1.
DR ROSITE; PS50835; IG_LIKE; 1.
ENCATTE; PS50835; IG_LIKE; IG_LIKE; II.
ENCATTE; PS50835; III.
ENCATTE; PS50835; III.
EN
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12316 MW; 0C3C38F81F1843CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
MEDLINE-73166638; PubMed-4700495;
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                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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   61
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Huber C., Klobeck H.G., Zachau H.G.;
"Ongoing V kappa-J kappa recombination after formation of a productive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr, Gaskin F., Fu S.M.;
"A rheumatoid factor from a normal individual encoded by VH2 and V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wagner S.D., Luzzatto L.; "Wagner S.D., Luzzatto L.; "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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   SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMZALQAPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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MEDLINE-98277139; PubMed-9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.4%; Score 484.5; DB 2; Length 114; 83.2%; Pred. No. 1e-42; ive 8; Mismatches 10; Indels 1
                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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Eur. J. Immunol. 22:1561-1565(1992).

EmBL; AR038034; AAD56270.1; -; mRNA.

PIR; B49002; B49002.

PIR; S23638; S23638.

PIR; S34094; S34094.

PIR; S34095; S34095.

HSSP; P01652; 11V4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kappa II gene segments.";
Arthritis Rheum. 35:900-904(1992).
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                QULBO_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 83.2
nes 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 somatic mutation."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=1322670;
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                                                                                                                                                                                       SOLITION TO BE A SECTION OF SECTI
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
11 kappa chain V-II region 26-10.

Mus musculus (Mouse).

Bukaryota: Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
MUroidea; Muridae; Mus.
11 maxid=10090;
                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Erlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.; "Studies of the interactions between the anticytokeratin 8 monoclonal annibody TS1, its antigen and its anti-idiotypic antibody alphaTS1."; J. Mol. Recognit. 16:157-163(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novotny J., Margolles M.N.;
"Amino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma antibody.";
Blochemietry 22:1153-1158-118919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHV-PWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SGVPDRPSGSGSGTDFTLKISRVEAEDLGVYFCSQTTHVPPYTFGGGTKLEMK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLECTIDE SEQUENCE.

Erlandsson A.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ884575; CAI56337.1; -; mRNA.

InterPro; IPR003599; Ig.

InterPro; IPR007110; Ig-like.

InterPro; IPR005596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 AA; 12560 MW; E4D3BF3D63E88007 CRC64;
                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.3%; Score 483.5; DB 2;
81.4%; Pred. No. 1.3e-42;
tive 12; Mismatches 8;
                                                                     10-MAY-2005 (TrEMBLrel. 30, Last sequence upd. 10-MAY-2005 (TrEMBLrel. 30, Last annotation upd. Kappa light chain variable region (Fragment). Name-1gGl anti-TS1 VL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 AA
                                                Created)
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MEDLINE=83178921; PubMed=6404298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF07686; V-set; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                10-MAY-2005 (TrEMBLrel. 30,
OSF210 MOUSE PRELIMINARY;
QSF210;
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                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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us-10-735-916a-65.rup

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rissum=Lung;
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                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Bolatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                             Gaps
 MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVPDRFSGSGSGTDFTLKISRVEAEDLGIYFCSQTTHVPPTFGGGTKLEIK 112
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                                                                                                                                                                                            Hybridoma; Immunoglobulin domain;
                                                                                                                                                                                                                              Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                       Length 113;
                                                                                                                                                                                                                                                       Complementarity-determining-2.
                                                                                                                                                                                                                                                                              Complementarity-determining-3.
Framework-4.
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                                                                                                                                                                                                                                                                                                                  113
12273 MW; F9F39CE949A84C2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                      81.0%; Score 482; DB 1;
81.2%; Pred. No. 1.8e-42;
                                                                                                                                                                                            Direct protein sequencing; Hybridoma; Immunoc
Immunoglobulin V region; Monoclonal antibody
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                                                                                                                   HSSP; Q99M37; 1191.
Ensembl; ENSMUSG00000055315; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR03596; Ig-v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                             Framework-2.
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            protein that binds digoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8TCDO_HUMAN PRELIMINARY;
Q8TCDO;
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nes 91; Conservative
                                                                                                         PIR; A01914; KVMS26.
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113 AA;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein R., Jaenichen R., Zachau H.G.; "Expressed human immunoglobulin kappa genes and their hypermutation."; Eur. J. Immunol. 23:3248-3262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wagner S.D., Luzzatto L.; "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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Hirabayashi Y., Munakata Y., Sasaki T., Sano H.;
Hariable regions of a human anti-DNA antibody O-81 possessing lupus
nephritis-associated idiotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=1551402;
Lautner-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F., Thiebe R., Zocher I., Zachau H.G.;
"The human immunoglobulin kappa locus. Characterization of the duplicated A regions.";
Eur. J. Immunol. 22:1023-1029(1992).
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PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG WHC; UNKNOWN 1.
Hypotherical protein; Immunoglobulin domain.
SEQUENCE 239 AA; 26235 WW; FACEDC3A3B03871D CRC64;
                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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80.4%; Pred. No. 7.2e-42;
ive 13; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Immunol. 23:391-397(1993).
EMBL; BC022362; AAH22362.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 20:2601-0(1992).
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig.MHC.
InterPro; IPR003596; Ig.v.
Pfam; PF07654; Cl-set; I.
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$40324; $40324.

$40374; $40374.

$42267; $42267.
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NUCLEOTIDE SEQUENCE.
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SMR; Q8TCD0; 2
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Q6PIH6 HUMAN
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Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A popkins R.F., Jordan H., Moore T., Mang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan K.J., Maske J.A., Gunzarne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska W.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Shoring C.M., Shoring C.M., Marra M.A.,
Shoring C.M., Shoring C.M., Marra M.A.,
Shoring C.M., Shoring C.M., Marra M.A.,
Shoring C.M., Margan M.A., Shoring C.M., Margan M.A.,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063299; AAH63599.1; -; mRNA.
HSSP; P01837; 1KCU.
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SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;
                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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80.4%; Pred. No. 9.1e-42;
                                                        239 AA
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                                                     QEP491_HUMAN PRELIMINARY;
Q6P491;
                                                                                                                                                                                        Hypothetical protein. Homo sapiens (Human).
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TISSUE=Skin;
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MEDINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MISTANDE R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Hilalon D.K., Muzny D.M., Sodersten B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butkeffeld Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerchion and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHV-PWTFGQGTKVEIK 112
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A Director MGC Project;

B Director MGC Project;

L Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC034142; AAH34142.1; -; mRNA.

R HSSP; P01837; 1MSB.

SMR; Q6PH6; 23-240.

R INTERPRO; IPR003599; Ig.

DR InterPro; IPR003109; Ig.-1; e.

DR InterPro; IPR003506; Ig. MHC.

DR InterPro; IPR003506; Ig. MHC.

DR InterPro; IPR003596; Ig. V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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SWART; SW00409; IG, 2.
SWART; SW00407; IGC1; 1.
SWART; SW00407; IGC1; 1.
PROSITE; PS00290; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 240 AA; Z6234 MW; 188D4DD8BB781EC4 CRC64;
                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                 240 AA.
             PRT;
                                                                    05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
QEPIHE_HUMAN PRELIMINARY;
QEPIHE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse cDNA sequences
                                                                                                                                                                                                                                               Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                          Name=IGKV1-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93;
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KV2A_HUMAN

RESULT 11

RESULT 12

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Kipp B., Schlaak M., Becker W.M.;
"Cloning and expression of a recombinant mouse Fab-fragment
recognizing a defined linear epitope of Chironomus thummi thummi major
allergen Chi t I.",
Int. Arch. Allergy Immunol. 110:348-353 (1996).
EMBL; Z37499; CAA85724-1; -; mRNA.
SMR; Q652C0; 1-219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIVMIQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                   a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCPQGIHVPYTFGGGTRLEIK 112
                                                                                    NUCLEOTIDE SEQUENCE.
MEDINE=8613012; Pubed=3937730;
01lier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
"The idiotypic network and the internal image; possible regul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.2%; Score 471; DB 2; Length 112; 80.4%; Pred. No. 2.6e-41;
                                                                                                                                                                                                                                                                                                                                                                                    (NOV-1986) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7E1B82A14EAF8445 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 AA; 12266 MW; C844B7881A89C18A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.4%; Pred. No. Live 10; Mismatches
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Q652C0;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequen
25-OCT-2004 (TrEMBLrel. 28, Last annota
Kappa light chain C_region (Fragment).
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STRAIN=Balb/c; TISSUE=Spleen;
MEDLINE=96319505; PubMed=8768802;
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X03386; CAA27113.1; -; mRNA.
NON_TER 1
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InterPro; IPR003599; IG.
InterPro; IPR003597; IG-11ke.
InterPro; IPR003597; IG_C1.
InterPro; IPR003596; IG_WHC.
InterPro; IPR003596; IG_WHC.
InterPro; IPR003596; IG_V.
Pfam; PF07654; C1-8et; I.
SMART; SM00407; IGC1.
SMART; SM00407; IGC1.
FROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE OF 108-109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90; Conservative
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Best Local Similarity
                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                        Fougereau M.;
Submitted (NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; B91639; KZHUCM.
HSSP; P01751; 1NQB.
SMR; P01614; 2-115.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0005576; P:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; 1g-11ke.
InterPro; IPR003196; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE; PSSO035; IG_LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular basis of antibody formation.";
Naturwissenschaften 56:195-205(1969).
-i- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-i- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 LYGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 AA; 12676 MW; 59E9F90A379569EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967)
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Last annotation update)
                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
18 kappa chain V-II region Cum.
Homo sapiens (Human)
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MEDLINE=70063440; Pubmed=4188189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
      PRT;
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=68242259; PubMed=5586923;
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Q53VPB MOUSE PRELIMINARY;
Q53VP8;
      STANDARD;
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   KV2A HUMAN
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                                           1 ELVMIQSPLSLSVSLGDQASISCRSSQSLVHINGNTYLHWYLQKPGLSPKLLIYIVSNRF 60
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                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Riesen W.F., Jaton J.-C.;
"Variable region sequence of the light chain from a Waldenstroms IgM with specificity for phosphorylcholine.";
Blochemistry 15:3829-3831(1976).
-I- MISCELLANBOUS: This chain was isolated from a Waldenstrom's
                                                                                    61 YGVPDRPSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVBIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Framework-3.
Complementarity-determining-3.
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 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00406; IGV; 1.—
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       macroglobulin that binds phosphorylcholine.
                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Imp kappa chain V-II region FR.
Homo sapiens (Human).
 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIRE TRANSP. (1991).
SMR; P01615; 1-109.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
                                                                                                                                                                                            113 AA.
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 89; Conservative
                                                                                                                                                                                           STANDARD;
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39
54
61
102
112
93
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SEQUENCE
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Db 61 SGVPDRFSDSGSGTDFTLKITRVQAEDVGVYYCMQATZSPYTFGQGTKLZIK 112
Search completed: January 10, 2006, 20:53:25
Job time: 75.5025 secs
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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
                   Copyright
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- protein search, using sw model OM protein Run on:

January 10, 2006, 20:28:02; Search time 13.5124 Seconds (without alignments) 797.508 Million cell updates/sec

US-10-735-916A-65 595 Perfect score:

1 DIVMTQSPLSLPVTPGEPAS......CFQGSHVPWTFGQGTKVEIK 112 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB @ Maximum DB @ Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
?: pir2:*
: pir3:*
: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ig light chain pre	ti-DNA autoan	g kappa	g light	light	ы	g kappa chain	g kappa chain	kappa	g kappa	g kappa	g kappa	kappa chain	g kappa	g kappa	g kappa chain	kappa	g kappa	g kappa chain	g kappa chain V-	kappa	g kappa	g kappa chain	g kappa chain	g kappa chain	chain	g light (g kappa chain	
SUMMARIES	ΩI	B39276	PL0203	S52028	S58207	838719	S40357	A31807	PC4203	S26335	A32967	PT0359	B34904	B31485	C27887	C34904	A27887	F27887	538715	S26882	B32967	S40342	E27887	KZHUGM	B30577	K2HURP	S16112	PH1043	ぜ	B32513
	DB	2	7	7	7	7	~	N	N	N	N	~	N	~	~	7	~	N	N	~	~	~	~	-	N	Н	7	N	~	7
	Length	131	113	219	112	112	136	112	219	110	114	118	131	112	112	131	112	112	115	132	114	135	112	117	131	133	219	103	131	131
d	Query Match	87.9	87.7	86.7	86.4	86.4	86.4	v	86.2	86.1	85.5	85.4	85.4	85.0	84.7	84.7	84.4	84.2	84.2	84.2	84.0	84.0	•	83.9	83.9	83.9	83.9	3	83.7	83.7
	Score	523	522	516	514	514	514	513	513	512	509	508	508	206	504	504	502	501	501	501	200	200	499	499	499	499	499	498	498	498
	Result No.		7	м	4	ហ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	29

kappa	kappa	kappa	kappa	ibody	light	kappa	Ig kappa chain pre	kappa	kappa	kappa	light	kappa	kappa	kappa	kappa
D28195	PL0257	A49715	840339	S53750	B41940	S32189	JL0029	822902	S40356	A24452	S58206	D27887	D29380	823230	B27887
~	~	7	0	7	~	7	7	0	N	Н	~	~	7	~	7
112	111	112	126	112	113	112	225	142	125	133	112	112	131	133	112
83.5	83.4	83.4	83.1	83.0	83.0	82.9	82.9	82.7	82.5	82.5	82.4	82.4	82.4	82.4	82.2
497	496	496	494.5	494	494	493	493	492	491	491	490	490	490	490	489
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Ig light chain precursor V-D-J region (6-19) - mouse

[5] Species: Mus musculus (house mouse)

[5] Species: Mus musculus (house mouse)

[6] Species: Mus musculus (house mouse)

[7] Species: Mus musculus (house mouse)

[7] Accession: B33276

[8] R. Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.

[8] R. Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.

[8] R. Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.

[8] R. Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.

[8] R. Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.

[8] R. Reininger, L.; Berney, T.; Shibata, T.; Shibata, T.; Spertini, F.; Mulb.2263605

[8] R. Reininger, L.; Berney, T.; Shibata, T.; Shibata, S.; Nibolecule type: mRNA

[8] R. Residues: 1-131 crsi.

[8] R. Residues: 1-131 crsi.

[8] R. Residues: 1-131 crsi.

[9] R. Residues: 1-
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		0; Gaps	1 DIVMTOSPLSLPVTPGEPASISCRSSOSIVHSNGNTYLQWYLQKPQQSPQLLIXKVSNRL 60	20 DVLANTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 79
			LELIY	TILIY
131;		6 0	OSPO III.	OSPK
87.9%; Score 523; DB 2; Length 131;		5; Indels	CLOKPG	/LOKPG
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2	42;	č.	ĮĮ.	TYLE
DB.	86.6%; Pred. No. 2.1e-42;	ea	EPASISCRSSOSIVHSNGNTYL	SNG
23;	0	Matches 97; Conservative 10; Mismatches	SIVE	SIVE
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RESULT 2

PLUZUS
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Puzus
C;Species: Puzus
C;Species: Puzus
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
Mol. Immunol. 27, 463-470, 1990
MyTitle: Variable region primary structures of monoclonal anti-DNA autoantibodies from N A;Reference number: PL0198; MUID:90309768; PMID:2114528
A;Accession: PLO203
A;Molecule type: mRNA
A;Residues: 1-113 <SMI>A;Residues: UNIPRAR:UPI0000113786; GB:X53643; NID:950196; PIDN:CAA37694.1; PID:9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology xIMMF;24-39/Region: complementarity-determining 1
F;94-102/Region: complementarity-determining 3
F;101-113/Region: D region

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A;Residues: 1-112 <CIM>
A;Residues: 1-112 <CIM>
A;Cross-references: UNIPARC: UPI0000117543; EMBL:X76021; NID:9416112; PIDN:CAA53608.1; PI.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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Ig kappa chain V region (PAC1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Jul-1989 #sequence_revision 20-Jul-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                        Ig light chain V region - mouse
C;Species: Whs musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C;Accession: $4031.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40357
A;Accession: $40357
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                                     61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPWTFGQGTKVEIK 112
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A;Cross-references: UNIPROT:QBNEKO; UNIPARC:UPI0000176CA8; EMBL:X72467
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61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 112;
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                                                                                                                                                                                                                                                                                                                                                         Richmanis, A.Y.
submitted to the EMBL Data Library, November 1993
A;Reference number: S38713
A;Acteresion: S38719
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
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C;Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>
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Ig kappa chain - mouse

C; Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Accession: 552028

R; Van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.; Submitted to the EMBL Data Library, August 1994

A; Description: Coordinate expression of antibody subunit genes yields high levels of fun A; Reference number: 552028

A; Accession: 552028

A; Accession: 552028

A; Accession: 552028

A; Residus: preliminary

A; Residus: 1-219 < VAN.

A; Residues: 1-219 < VAN.

A; Croser-references: UNIPARC: UPI0000114B22; EMBL: L35138; NID: G522336; PIDN: AAA67525.1; PIC; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Reywords: heterotetramer; immunoglobulin

F; 16-95/Domain: immunoglobulin homology < INM.
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000
C;Accession: S58207
R;Welschof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, submitted to the EMBL Data Library, July 1995
A;Description: Characterization of heavy and light chain immunoglobulin variable region A;Reference number: S58206
A;Accession: S58207
A;Accession: S58207
A;Accession: S58207
A;Accession: S58207
A;Accession: S68206
A;Accession: S68207
A;Accession: S68207
A;Accession: S68207
A;Cross-references: UNIPARC:UPI0000116253; EMBL:X89056; NID:g929642; PIDN:CAA61443.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
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                                 Length 113;
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                              87.7%; Score 522; DB 2;
86.6%; Pred. No. 2.3e-42;
iive 10; Mismatches 5;
                                                             Local Similarity 86.6%
les 97; Conservative
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Ig kappa chain V region (R4A.12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Shefner, R.; Kleiner, G.; Turken, A.; Papazian, L.; Diamond, B. J. Exp. Med. 173, 287-296, 1991
A;Title: A novel class of anti-DNA antibodies identified in BALB/c mice. A;Reference number: PT0352; MUID:91108325; PMID:1988536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 508; DB 2; Length 118; ; Pred. No. 5e-41; 10; Mismatches 8; Indels
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C, Comment: This protein is an anti-double-stranded DNA antibody
C, Superfamily: immunoglobulin V region; immunoglobulin homology
F, 19-98/Domain: immunoglobulin homology < IMM>
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Best Local Similarity 83.9%;
Matches 94; Conservative 1
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Best Local Similarity
Matches 95: Conserv
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Best Local Similarity
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C;Accession: DC4203
R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mc
A;Reference number: PC4202; MUID:97082978; PMID:8964510
A;Reference number: PC4203
A;Rolecule type: mRNA
A;Residues: 1-219 cKWA>
A;Cross-references: UNIPARC:UPIO0001157E4; GB:U29147; NID:g1594225; PIDN:AAC52821.1; PIC
C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: V region #status predicted cCRG>
F;113-219/Domain: C region #status predicted cCRG>
C;Accession: A31807
R;Taub, R.; Gould, R.J.; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shatt B;Taub, R.; Gould, R.J.; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shatt A; Esol. 264, 259-265, 198
A;Title: A monoclonal antibody against the platelet fibrinogen receptor contains a seque A;Reference number: A31807
A;Reference number: A31807
A;Accession: A31807
A;Accession: A31807
A;Accession: A31807
A;Accession: A31807
A;Accession: A31807
A;Accession: A31807
C;Superferences: UNIPARC: UPI00001424F9
C;Superferences: UNIPARC: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <INM>
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C;Species: Mus musculus (house mouse)
C;Date: 13.4an-1995 #sequence_revision 13.7an-1995 #text_change 20.Jun-2000
C;Accession: 226335
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-224, 1991
J. Exp. Med. 174, 613-224, 1991
A;Reference mumber: S26309; MUID:91341421; PMID:1908510
A;Accession: S26335
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;Species: Mus musculus (house mouse)
;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-110 <STA>
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A;Cross-references: UNIPARC:UPI0000115F78; EMBL:X59183; NID:g52314; PIDN:CAA41893.1; PIC C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 21-Jan-2000
C;Accession: A32967
C;Accession: A32967
Elbevy, R; Assulin, O.; Scherf, T.; Levitt, M.; Anglister, J.
Biochemistry 28, 7168-7175, 1889
A;Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, preda
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A;Residues: 1-114 <LEV>
A;Cross-references: UNIPARC:UPI0000114F5D; GB:M30481; NID:g197157; PIDN:AAA38935.1; PID
A;Cross-references: UNIPARC:UPI0000114F5D; GB:M30481; NID:g197157; PIDN:AAA38935.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heteroretramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 21-Jan-2000
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83.0%; Pred. No. 3.8e-41;
ive 13; Mismatches 6; Indels
                                                                                                                                                                           Length 110;
                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                       ch 86.1%; Score 512; DB 2; 1 Similarity 86.4%; Pred. No. 1.9e-41; 95; Conservative 10; Mismatches 5;
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us-10-735-916a-65.rpr

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C;Accession: C27887
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
R;MoJ J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a G. A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: C27887
                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-112 < CAT)-
A; Cross-references: UNIPROT:Q8VCI6; UNIPARC:UPI0000176A17
A; Experimental source: strain Balb/c
A; Note: this sequence was determined from the germline gene
C; Comment: This chain was isolated from a hybridoma protein that binds influenza virus his
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology < LMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain precursor V region (3-24) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
C;Accession: (34904; I31485
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
A;Eldle: Active site structure and antigen binding properties of idiotypically cross-rear A;Reference number: A34903; MuID:90094387; PMID:2104617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: mRNA
A,Residues: 1-131 - ABD.
A,Gross-references: UNIPROT:08VCI6; UNIPARC:UBI00001767A8
R,Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
C, Biol. Chem. 264, 1565-1569, 1989
A,Title: Comparison of variable region primary structures within an anti-fluorescein idia
A,Reference number: A31485; MUID:89109167; PMID:2492278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 DVVMTQTPLSLEPVSLGDQASFSCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF 79
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                                                          Ig kappa chain V region (H37-82) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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83.0%; Pred. No. 1.1e-40;
ive 11; Mismatches 8; Indels
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84.7%; Score 504; DB 2; Length 13
Best Local Similarity 83.0%; Pred. No. 1.3e-40;
Matches 93; Conservative 10; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93; Conservative
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B31485
IG Wappa chain V region (4-4-20) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 09-Jul-2004
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 09-Jul-2004
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 09-Jul-2004
C;Date: 31-Jul-1989 #sequence_revision 31485
R;Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J; Biol. Chem. 264, 1565-1569, 1989
A;Title: Comparison of variable region primary structures within an anti-fluorescein idi
A;Reference number: A31485; MUID:89109167; PMID:2492278
A;Accession: B31485
A;Accession: Bylaniaray
A;Molecule type: protein
A;Residues: 1-112 <BED>
A;Cross-references: UNIRROT:Q8VCI6; UNIRARC:UP10000176AF8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IVM+>
                                                                                                                                                                                                                                                                         RESULT 12
B34904
Ig kappa chain precursor V region (12-40 and 5-14) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C;Accession: B34304; #134903
R;Bedzyk, W.D.; Herron, J.N.; Edmudson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-rea
A;Reference number: A34903; MUID:90094387; PMID:2104617
A;Accession: B34904
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-131 < ABED>
A;Cross-references: UNIPARC:UPI0000114FC8; GB:M32384; GB:J05237; GB:J05238; NID:g639656;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>
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   DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                              63
                                    DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGOSPKLLIXKVSNRP
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                                                                                                                            61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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1 Similarity 83.9%; Pred. No. 5.6e-41;
94; Conservative 10; Mismatches 8; Indels
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83.0%; Pred. No. 7.2e-41;
ive 12; Mismatches 7; Indels
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Best Local Similarity
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Best Local S.
Matches 93
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January 10, 2006, 20:07:41; Search time 77.3134 Seconds (without alignments) 636.505 Million cell updates/sec
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1 DIVMTQSPLSLPVTPGEPAS......CFQGSHVPWTFGQGTKVEIK 112
5.1.6
Compugen Ltd.
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 GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                                             - protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Adj76899 Anti-IGF-	Adz67069 Human ant	Adj76901 Anti-IGF-		Adj76895 Anti-IGF-		Adj76897 Anti-IGF-	_	Adp84950 Variable	_	Adp84948 Variable	-		•			-	Adp84949 Variable	_		Ade36523 Anti-FGF-	0	Adp84947 Variable	Aay42969 Humanised
SUMMARIES		ΙD	ADJ76899	ADZ67069	ADJ76901	ADZ67071	ADJ76895	ADZ67065	ADJ76897	ADZ67067	ADP84950	AAE15713	ADP84948	AAE15712	ABP72125	ADE36495	ADP84946	ADP84951	ADE36530	ADP84949	AAE15711	ADP84944	ADE36523	AAY42960	ADP84947	AAY42969
		图:	7	σ	7	σ	7	σ	7	σ	œ	'n	œ	ß	9	7	8	œ	7	8	ß	œ	7	7	œ	7
		Length DB	112	112	131	131	112	112	131	131	114	112	114	112	112	112	114	114	131	114	112	114	112	112	114	132
	* Query	Match	100.0	100.0	100.0	100.0	99.8	8.66	99.8	99.8	95.8	95.3	95.1	94.8	94.8	94.8	94.8	94.8			94.5		•	93.9	93.9	•
		Score	595	595	595	595	594	594	594	594	570	567	266	564	564	564	564	564	564	563	562	260	559	559	559	559
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Aar32239 Humanised	Aaw27145 Mature li	Aay87571 Humanised	Ade36522 Anti-FGF-	•	_	-	Adv67310 Amino aci		Adp84943 Variable		Adj80420 Hybrid hu	Adh61998 Human ant	Abr40268 Amino aci	Ade27687 Humanised		Adj80422 Murine an	Adz52545 Anti-CCR4	Aea33234 CC chemok	Abr40272 Amino aci	Ade27694 Humanised
AAR32239	AAW27145	AAY87571	ADE36522	ADP84945	ABP72129	ADE36520	ADV67310	ADP84952	ADP84943	ADE36518	ADJ80420	ADH61998	ABR40268	ADE27687	ADE36527	ADJ80422	ADZ52545	AEA33234	ABR40272	ADE27694
2	2	3	2 7	4 8	2	2 7	5	4 8	4 8	2 7	2 7	2 7	2 6	2 7	2 7	2 7	2 9	2 9	2 6	2 7
11	11	11	11	11	11	11	11	11	11	11	11	13	11	11	11	11	11	112	11	11
93.6	93.6	93.6	93.6	93.6	93.4	93.4	93.4	93.4	92.9	92.8	92.3	92.3	91.9	91.9	91.9	91.9	91.9	91.9	91.8	91.8
557	557	557	557	557	556	556	556	556	553	552	549	549	547	547	547	547	547	547	546	546
25	26	27	28	29	30	31	32	33	34	35	36	3.7	80	3 6	40	41	42	43	44	45

ALIGNMENTS

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or-2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers. Disclosure; SEQ ID NO 65; 164pp; French. cytostatic; antipsoriatic; antibody; (FABR) FABRE MEDICAMENT SA PIERRE. ADJ76899 standard; protein; 112 AA Anti-IGF-1R related protein #14. Leger O; 18-JAN-2002; 2002FR-0000653. 18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-0005753. 20-JAN-2003; 2003WO-FR000178. 06-MAY-2004 (first entry) Goetsch L, Corvaia N, WPI; 2003-569653/53 WO2003059951-A2. Homo sapiens 24-JUL-2003. ADJ76899; ADJ76899

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RESULT 3
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            transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                    neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obsterincs; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
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                                                                                                                                                      1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                     Human antibody 7C10 2 light chain variable region SEQ ID NO:65.
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                                                                                                            Length 112;
receptors with their ligands. Especially they inhibit
                                                                 protein sequence used to generate the Ab of the invention
                                                                                                                               Indels
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                                                                                                           100.0%; Score 595; DB 7; 100.0%; Pred. No. 2.5e-43;
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                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                       ADZ67069 standard; protein; 112
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18-JAN-2002; 2002FR-0000554.

07-MAY-2002; 2002FR-00005753.

20-JAN-2003; 2003WO-FR000178.
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                                                                                                                                                                                                                                                                                                                                                                                                                          chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for treating cancer.
                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                     Best Local Similarity 100.
Matches 112; Conservative
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CORVAIA N.
LEGER O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAEUW J.
                                                                                       Sequence 112 AA;
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                                                                                                            Query Match
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(LEGE/)
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(HAEU/)
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Treeperor (IGF-IR) antibody (I) or its functional fragment, being capable of capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of apable of the human IGF-IR and, if necessary, capable of apable of capable of binding to human IGF-IR and, if necessary, capable of determining region (CMF) consisting of one of two fully defined is amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or Connected with a ctivation of the IGF-IR and/or EGFR, and/or connected with a ctivation of the IGF-IR and/or EGFR, and/or connected with cinduce or only slightly interaction of the medicament does not induce or only slightly induced to IGF-IR and/or EGF-With IGF-IR and/or EGF-With IGF-IR and/or IGF-With IGF-IR and/or IGF-With IGF-IR and/or IGF-With IGF-IR and/or IGF-With IGF-With
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relates to a novel isolated anti-insulin-like growth factor
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74. .80 /note= "CDR2" 113. .121

Region Region

/note= "CDR3"

US2005084906-A1

21-APR-2005

18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-00005753. 20-JAN-2003; 2003WO-FR000178. 11-JUL-2003; 2003FR-00008538.

GOETSCH L. CORVAIA N. LEGER O. DUFLOS A. HAEUW J.

(GOET/)

BECK A.

(BECK/)

(DUFL/)
(HAEU/)

(LEGE/)

2002FR-00000653

18-JAN-2002;

16-DEC-2003; 2003US-00735916

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                                                                                                                                                                                                                                                                                          The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR. Ab and its fragments are used to prevent or IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of tumor cells, so are useful against cancers of the prostate. Unuy, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; light chain variable region.
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                                                                                                                                                                                                        New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein sequence used to generate the Ab of the invention

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    /note= "leader peptide"

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                                  18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
 20-JAN-2003; 2003WO-FR000178.
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Matches 112; Conservative
                                                                                                                                       Goetsch L, Corvaia N,
                                                                                                                                                                          WPI; 2003-569653/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 131 AA;
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CRR) consisting of one of two fully defined is amino acids (ADSG/006 and ADSG/014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal approactivation of the transduction pathway of the signal mediated by the intended of IGF-IR and/or EGER, and/or of EGER, with EGE-IR and/or EGER, and/or of EGER, with EGE-IR and/or EGER, and antibody of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin record intended and antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF and/or IGF2.

Capandent and/or EGF-dependent and/or HERZ/neu-dependent and/or intended for preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or IGF2 and/or the proliferation of a medicament intended for the preparation of a medicament intended for the prostate cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the specific targeting of a bill preses induced by active compound to the preparation of a medicament intended for the specific targeting of a bill preses induced by a subsensing or overexpr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                       Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) artibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
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           Beck
Leger O, Duflos A, Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 12; SEQ ID NO 67; 125pp; English.
           Corvaia N,
                                                                                                                        WPI; 2005-321968/33.
                                                                                                                                                                                 N-PSDB; ADZ67070
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/note= "CDR1"

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Region

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Gaps

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Indels

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                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; antipsoriatic; antibody; IGF-1R; tyrosine kinase activity; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                       DIVMIQSPLSLPVIPGEPASISCRSSQSIVHSNGNIYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                Gaps
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                                                                                                                                                                    80 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGGGTKVEIK 131
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               Length 131;
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               Score 595; DB 9;
Pred. No. 3e-43;
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Pred. No. 3.1e-43;
100.0%; Scor.
100.0%; Pred. No. 30.
0; Mismatches
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                                                                                                                                                                                                                                                                   ADJ76895 standard; protein; 112 AA
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                                                                                                                                                                                                                                                                                                                                                                    Anti-IGF-1R related protein #12.
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18-JAN-2002; 2002FR-0000654.
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99.1%;
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                               Local Similarity 100.
1es 112; Conservative
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Best Local Similarity
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Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lump tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGP-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                        1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                             YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIX 112
                                                                                                                                                                                                                    Human antibody 7C10 1 light chain variable region SEQ ID NO:61.
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                                                                                                                                          ADZ67065 standard, protein; 112
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2002FR-00000654.
2002FR-00005753.
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94. .102
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/note= "CDR3"
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CORVAIA N.
LEGER O.
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comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of the preparation of the IGP-IR and/or connected with a cativation of the IGP-IR and/or EGFR, and/or connected with a cativation of the IGP-IR and/or CDR6FR, where the administration of the reasolution pathway of the signal mediated by the interaction of IGF or IGP2 with IGF-IR and/or of EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin control inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2.

CC dependent and/or EGF-dependent, especially IGF1 and/or IGF2.

CC dependent and/or EGF-dependent and/or HER2/neu-dependent calls. (I) is useful for preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcome, lung cancer, che cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for prevention or for the prevention or a medicament colls. (I) is useful in preparation of a medicament colls or preparation of a proper colls o
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  specifically inhibiting tyrosine kinase activity of the receptor,
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99.1%; Pred. No. 3.1e-43;
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or creat diseases associated with overexpression and/or abnormal activity of IGF-IR. Ab and its fragments are used to prevent or IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neoplasm; prostate tumor; andrology; genitourinary disease, osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gyneocology and obstetrics; breast tumor; endometroid carcinoma; gastrointesinal disease; colon tumor; antipporiatic; psoriasis; dermatological disease; immune disorder;
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                                                                                                                                                               New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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Pred. No. 3.6e-43;
1; Mismatches 0; Indels
                                                                                                                                                                                                                     Disclosure; SEQ ID NO 63; 164pp; French.
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                                                     (FABR ) FABRE MEDICAMENT SA PIERRE.
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
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99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.1
Matches 111; Conservative
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                                                                                          Corvaia N,
                                                                                                                           WPI; 2003-569653/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 131 AA;
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                                                                                          Goetsch L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADZ67067;
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/note= "CDR3"

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Treeptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of eapable of binding to human IGF-IR and, if necessary, capable of capable of binding tyoshine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGF-IR and/or EGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induced by the interaction of IGPI or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induced secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the grant and/or EGF-dependent and/or HERZ/neu-dependent and/or EGF-dependent and/or HERZ/neu-dependent and/or IGF2-dependent and/or HERZ/neu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of psoriaals (I) is useful in the preparation of a medicament intended for prevention or colon cancer. (I) is useful in the preparation of a medicament intended for the specific targeting of a biologically active compound to intended for the specific targeting of a biologically active compound to intended for the specific targeting of a biologically active compound to intended in virture of in virtor diagnosis of illnesses induced by an inventor of intended of an intended in the IGF-IR and/or EGF IR and/or CIRZ-IR and/or EGF IR EGF IR and/or EGF IR EARD-IR ALL ALL EGF IR EARD-IR EGF IR EARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duflos A, Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 12; SEQ ID NO 63; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leger O,
                                                                                                                                                                              2002FR-00000653
                                                                                                                                                                                                   2002FR-00000654.
                                                                                                                                                                                                                                             20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                  16-DEC-2003; 2003US-00735916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2005-321968/33.
                                                                                                                                                                                                                                                                                                              GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                DUFLOS A. HAEUW J.
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                                            US2005084906-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                BECK A.
                                                                                                                                                                              18-JAN-2002;
                                                                                                                                                                                                                          07-MAY-2002;
                                                                                        21-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goetsch L,
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(HAEU/)
                                                                                                                                                                                                                                                                                                                                                                                                                              (BECK/)
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Score 594; DB 9; Pred. No. 3.6e-43; 99.8%; Query Match Best Local Similarity

Length 131;

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This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition molecules are used to make constructs containing the framework regions that separate, include and/or flank the specified sequences, especially where the framework regions are from the immunoglobulin (Ig) superfamily, protease inhibitors. Lectims, helix-bundle proteins and/or lipocalins. Most especially the framework regions are from antibodies, particularly the variable heavy chain (WH) and the variable light chain (VL) of human and/or mutine origin. The constructs may also include a His or myc tag, a lysine-rich region and/or a multimerisation domain, most particularly it is a single-chain antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment with peptide or protein, and/or an Ig of types G, M, A, E or D and/or their subclasses. It may be human, the humanised, murine or chimeric, e.g. IgM without the J chain. The additional sequences/structures in the constructs are Ig domains of various species, interacting or stabilising domains, signal sequences, fluorescent dyes, toxins, antibodies with catalytic activity or other specificities, sycylytic agents, enzymes, immuno-modulators or effectors, MHC molecules, antigens, chelators for radioactive labels, liposomes, transmembrane domains, viruses and/or cells, specifically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recognition molecules, e.g. antibodies (and nucleic acids) that bind specifically to Core-1 antigens, useful for diagnosis, treatment and prevention of tumors and metastases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protease inhibitor; lectin; helix-bundle protein; lipocalin; diagnosis; variable heavy chain; Wi; vaccine; diagnosis; alleviation; treatment; tumour; breast; colon; stomach; pancreas; large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody; Core-1 antigen; framework region; immunoglobulin superfamily;
                                                                                 20 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                         1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
  Gaps
                                                                                                                             YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFOGSHVPWTFGOGTKVEIK 112
                                                                                                                                                80 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPWTFGQGTKVEIK 131
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  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Variable light chain VL fragment Karo24 SEQ ID NO 92.
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  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; SEQ ID NO 92; 136pp; German.
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                                                                                                                                                                                                                                                                           ADP84950 standard; protein; 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2003; 2003WO-DE003994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-2002; 2002DE-01056900
                                                                                                                                                                                                                                                                                                                                                               09-SEP-2004 (first entry)
  Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-461095/43.
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Christensen PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metastasis.
                                                                                                                                                                                                                                                                                                                       ADP84950;
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                                                                                                                                                                                                                                    RESULT 9
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(SCAN-) SCANCELL LTD.

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            acid encoding them, and related vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment, monitoring and/or secondary treatment of tumours (specifically of breast, colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or liver) and/or metastases (particularly to liver), specifically where these are positive for the Ci antigen. The products of the invention provide simple, reliable and efficient detection of tumours. They are specific for carcinoma and show almost no binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; humanised form; monoclonal antibody alpha 140; gene therapy; epidermal growth factor receptor; BGF; cancer; colorectal; lung; breast; gastric; ovarian; immune response; cytostatic; cell growth; apoptosis; inhibitor; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                    1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRF 60
macrophages. The antibodies, also constructs containing them, nucleic
                                                                                                                                                                                                                                                                                  1 DIVMIQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                       61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                          61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPYTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse monoclonal antibody alpha 340 Vk region variant, 340VKd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Wild type Asn substituted with Lys"
                                                                                                                                                                                                                Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Wild type Asp substituted with Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Wild type Gln substituted with Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Wild type Leu substituted with Val"
                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Wild type Ser substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Wild type Leu substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Wild type Leu substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Wild type Lys substituted
                                                                                                                                                                                                                 Score 570; DB 8;
Pred. No. 3.5e-41;
2; Mismatches 2
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7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE15713 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAY-2000; 2000GB-00011981
24-AUG-2000; 2000GB-00020794
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                                                                                                                                                                                                                 Query Match
Best Local Similarity 96.4%;
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                  Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                   healthy tissue.
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE15713;
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
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nouse monoclonal antibody which binds to epidermal growth factor (EGF)
receptor and inhibits binding of EGF), obtainable from the cell line
deposited with the ECACC under accession number 97021428. The humanised
coposited with the ECACC under accession number 97021428. The humanised
corm of the antibody 340 is useful in gene therapy, medicine and in the
manufacture of a medicament for treatment or prophylaxis of cancer. The
invention is useful for treating colorectal, lung, breast, gastric or
covarian cancers or also for preventing the recurrence of cancer after
initial treatment or surgery. The invention is also useful for enhancing
a protective immune response against cancer by optimised immunisation
schedules. The humanised form of the antibody 340 has reduced
immunogenicity but shows similar binding to cells expressing EGF
receptor, as the original murine antibody and has increased ability to
inhibit the growth of EGF receptor expressing cells. The invention is
used as cell growth and apoptosis inhibitor. The present sequence is
mouse monoclonal antibody alpha 340 deimmunised light chain variable (VK)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                         New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                      present invention relates to a humanised form of the antibody 340 (a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody; Core-1 antigen; framework region; immunoglobulin superfamily; procease inhibitor; lectin; helix-bundle protein; lipocalin; variable heavy chain; VI; varcine; diagnosis; alleviation; treatment; tunour; breast; colon; stomach; panoreas; large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCFQGSHVPWTFGGGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 567; DB 5; Length 112;
Pred. No. 6.3e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Variable light chain VL fragment Karoll SEQ ID NO 90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP84948 standard; protein; 114 AA
                                                                                                                                                                                        Example 2; Fig 7; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2003; 2003WO-DE003994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-2002; 2002DE-01056900.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 105; Conservative
                                   Durrant LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region variant, 340VKd
                                                                         WPI; 2002-062384/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004050707-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUN-2004.
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                                   Ellis JRM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP84948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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inhibitor; mutant; mutein; variant.

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This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition molecules are used to make constructs containing the framework regions that separate, include and/or flank the specified sequences, especially where the framework regions are from the immunoglobulin (4g) superfamily, protease inhibitors, lectins, helix-bundle proteins and/or lipocalins. Most especially the framework regions are from antibodies, particularly the variable heavy chain (7H) and the variable light chain (VL) of human and/or murine origin. The constructs may also include a His or myc tag, is a single-chain antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment, multibody, Fab fragment, in advocable and/or an ig of the variable sequences/structures in the constructs are Ig domains of various species, interacting or stabilising domains, signal sequences, considering analytic activity or other analytic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specificities, cyanis, autinodies with catalytic activity or other specificities, cytolytic agents, enzymes, immuno-modulators or effectors, MrC molecules, antigens, chelators for radioactive labels, liposomes, transmembrane domains, viruses and/or cells, specifically macrophages. The antibodies, also constructs containing them, nucleic acid encoding them, and related vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment, monitoring and/or secondary treatment of tumours (specifically of breast, colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or liver) and/or metastases (particularly to liver), specifically where these are positive for the Cl antigen. The products of the invention provide simple, reliable and efficient detection of
                                                                                                                                                                                                                                                                                                    New recognition molecules, e.g. antibodies (and nucleic acids) that bind specifically to Core-1 antigens, useful for diagnosis, treatment and prevention of tumors and metastases.
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                                                                                                                  Stahn R;
                                                                                                              Danielczyk A, Karsten U, Ravn P,
                                   (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; SEQ ID NO 90; 136pp; German.
                                                                                                                                                                                                                         WPI; 2004-461095/43.
                                                                                                                                                      Christensen PA;
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1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60 0; Gaps Score 566; DB 8; Length 114; Pred. No. 7.8e-41; 3; Mismatches 2; Indels 95.1%; Query Match
Best Local Similarity 95.5;
Matches 107; Conservative Sequence 114 AA; ሯ

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61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCFQGSHVPYTFGQGTKVEIK 112

1 DIVMIQSPLSLPVIPGEPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIXKVSNRF

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AAE15712 standard; protein; 112 AA. AAE15712; AAE15712

(first entry) 12-MAR-2002

Mouse; humanised form; monoclonal antibody alpha 340; gene therapy; epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast; gastric; ovarian; immune response; cytostatic; cell growth; apoptosis; Mouse monoclonal antibody alpha 340 Vk region variant, 340VKc.

The present invention relates to a humanised form of the antibody 340 (a mouse monoclonal antibody which binds to epidermal growth factor (EGF) receptor and inhibits binding of EGF), obtainable from the cell line deposited with the ECACC under accession number 97021428. The humanised form of the antibody 340 is useful in gene therapy, medicine and in the convertion is useful for treatment or prophylaxis of cancer. The invention is useful for treating colorectal, lung, breast, gastric or ovarian cancers or also for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing a protective immune response against cancer by optimised immunisation schedules. The humanised form of the antibody 340 has reduced immunogenicity but shows similar binding to cells expressing EGF receptor, as the original murine antibody and has increased ability to contain the growth of EGF receptor expressing cells. The invention is cused as cell growth and apoptosis inhibitor. The present sequence is mouse monoclonal antibody alpha 340 deimmunised light chain variable (VK) cregion variant, 340VKc New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer. note= "Wild type Thr substituted with Ser" note= "Wild type Ser substituted with Thr" note= "Wild type Leu substituted with Pro" note= "Wild type Asp substituted with Glu" note= "Wild type Gln substituted with Pro" note= "Wild type Leu substituted with Thr" note= "Wild type Ile substituted with Val" /note= "Wild type Leu substituted with Val" /note= "Wild type Asn substituted with Lys" note= "Wild type Lys substituted with Location/Qualifiers Example 2; Fig 7; 53pp; English 21-MAY-2001; 2001WO-GB002226. 19-MAY-2000; 2000GB-00011981. 24-AUG-2000; 2000GB-00020794. Durrant LG; (SCAN-) SCANCELL LTD WPI; 2002-062384/08. Misc-difference 109 Misc-difference 112 Misc-difference 14 Misc-difference 15 Misc-difference 18 Misc-difference 50 Misc-difference 17 Sequence 112 AA; Misc-difference Misc-difference Misc-difference WO200188138-A1 22-NOV-2001 Ellis JRM, Mus sp. Synthetic.

1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60

Query Match 94.8%; Score 564; DB 5; Length 112; Best Local Similarity 93.8%; Pred. No. 1.1e-40; Matches 105; Conservative 3; Mismatches 4; Indels

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Gaps

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Uchii M,
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                 WO2003057251-A1.
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                                               Unidentified
                                                                                    17-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel humanised antibodies and antibody fragments which react with fibroblast growth factor 8 (FGF8) and inhibit its biological functions. The polypeptides of the invention have cytostatic activity. The antibody is useful for the treatment of cancer, including prostate, breast, ovarian and testicular cancer. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
          DVLMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLEWYLQKPCQSPQLLIYKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-FGP-8 (sic fibroblast growth factor) antibody-related protein #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                           Humanised antibodies and antibody fragments reacting with fibroblast growth factor 8 useful for the treatment and diagnosis of cancer.
Humanised, antibody, fibroblast growth factor 8; FGF8; cytostatic,
cancer; prostate; breast; ovarian; testicular.
                          61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPYTFGQGTKVEIK 112
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Pred. No. 1.1e-40;
4; Mismatches 2; Indels
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                                                                                              ABP72125 standard; protein; 112
                                                                                                                                                      FGF-8 related protein SEQ ID 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE36495 standard; protein; 112
                                                                                                                                                                                                                                                             28-JUN-2002; 2002WO-JP006591.
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Best Local Similarity 94.6
Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                          WPI; 2003-239169/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 112 AA;
                                                                                                                                                                                                                        WO2003002608-A1
                                                                                                                                   03-JUN-2003
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1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises a method for treating and preventing arthritis, the method involves the use of anti-FGF-8 (sic fibroblast growth factor) antibody. The antibody and method of the invention is useful for: the detection, treatment and prevention of arthritis; as a cartilage protection agent; as a joint destruction inhibitor; and as a synoviral proliferation inhibitor. The present amino acid sequence represents a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprising the use of anti-FGF-8
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Pred. No. 1.1e-40;
4; Mismatches 2; Indels
arthritis; anti-FGF-8; sic fibroblast growth factor; cartilage protection agent; joint destruction inhibitor; symoviral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variable light chain VL fragment Karo18 SEQ ID NO 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment and prevention of arthritis or (sic fibroblast growth factor) antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; SEQ ID NO 19; 193pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miki I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP84946 standard; protein; 114 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suda T,
                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2001; 2001JP-00400677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KYOW ) KYOWA HAKKO KOGYO KK
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This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition concletules are used to make constructs containing the framework regions are from the immunoglobulin (1g) superfamily, where the framework regions are from the immunoglobulin (1g) superfamily, protease inhibitors, lectins, helix-bundle proteins and/or lipocalins. Most especially the framework regions are from antibodies, particularly the variable heavy chain (14) and the variable light chain (11) of human and/or murine origin. The constructs may also include a His or myc tag, a lysine-rich region and/or a multimerisation domain, most particularly it is a single-chain antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment with peptide or protein, and/or an Ig of types G, M, A, E or D and/or their subclasses. It may be human, conversed, murine or chimeric, e.g. IgM without the J chain. The additional sequences/structures in the constructs are Ig domains of additional sequences/structures in the constructs are Ig domains of specific ities, cytolytic agents, enrymes, immuno-modulators or specificities, cytolytic agents, enrymes, immuno-modulators or effectors, MHC molecules, antibodies with catalytic activity or other specificities, cytolytic agents, enrymes in fine and/or cells, specifically or prevention (e.g. as vaccine), diagnosis, alleviation, treatment. Cc acid encoding them, and related vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment. Cc acid encoding them, and related vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment. Cc colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or superive and post cells, related encoding to prostate, kidney and/or metastases (particularly where these are positive for the Cl antigen detection of the invention provide simple, related encoding the prostate of particularly we
                                                                                                                                                                                                                                                                                                                             New recognition molecules, e.g. antibodies (and nucleic acids) that bind specifically to Core-1 antigens, useful for diagnosis, treatment and
                                                                                                                                                                                        Danielczyk A, Karsten U, Ravn P, Stahn R;
                                                                                                                                  (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; SEQ ID NO 88; 136pp; German
                                                                                                                                                                                                                                                                                                                                                                                   prevention of tumors and metastases.
                            01-DEC-2003; 2003WO-DE003994.
                                                                               29-NOV-2002; 2002DE-01056900
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                                                                                                                                                                                     Goletz S, Danie
Christensen PA;
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Sequence 114 AA;

ö 1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60 0; Gaps 94.8%; Score 564; DB 8; Length 114; 95.5%; Pred. No. 1.2e-40; ive 2; Mismatches 3; Indels Query Match Best Local Similarity 95.5' Matches 107; Conservative a ઠે

1 DIQMIQSPLSLPVIPGEPASISCRSSQSIVHSNGNIYLEWYLQKPGQSPQLLIYKVSNRF 60

8 셤 Search completed: January 10, 2006, 20:44:15 Job time: 78.3134 secs

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GENERAL INVOCATION

GENERAL INVOCATION

GENERAL INVOCATION

APPLICANT: CORVAIA, NATHALIB

APPLICANT: CORVAIA, NATHALIB

APPLICANT: CORVAIA, ALAIN

APPLICANT: HEGER, OLIVIER

APPLICANT: HEGER, OLIVIER

APPLICANT: HEGER, OLIVIER

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION NUMBER: US/11/012,353

CURRENT FILING DATE: 2003-12-16

PRIOR PILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 162

SOSTWARRE: PRECENTION OF 3.3
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100.0%; Pred. No. 2.5e-40;
ive 0; Mismatches 0;
US-10-932-334-86
US-10-932-334-90
US-10-932-334-90
US-10-512-184-65
US-10-512-184-66
US-10-512-184-66
US-10-932-334-10
US-10-932-334-10
US-10-932-334-84
US-10-932-334-82
US-10-932-334-82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 61, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
        Matches 112; Conservative
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US-11-012-353-61
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166.558 Million cell updates/sec
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595
1 DVVMTQSPLSLPVTPGEPAS......CFQGSHVPWTFGQGTKVEIK 112
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/cgn2_6/ptodata/1/pubpaa/USO7_NEW_FUB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCT_NEW_FUB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCT_NEW_FUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO7_NEW_FUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO1_NEW_FUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO1_NEW_FUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO1_NEW_FUB.pep:*
                                GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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                                            | PUDITICATION NO. US20050249730A1 |
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| APPLICANT: GORYSCH, LILIANE |
| APPLICANT: GORYSCH, LILIANE |
| APPLICANT: GORYSCH, LILIANE |
| APPLICANT: HAEUW, JEAN-FRANCSIS |
| APPLICANT: HEGER, OLIVIER |
| APPLICANT: HOWER: US ANTIBODIES AND USES THEREOF |
| FILE REPRESENCE: 0.17753-198 |
| FILE REPRESENCE: 0.17753-198 |
| FRICH REPLICATION NUMBER: FR 0308538 |
| PRIOR FILING DATE: 2003-01-10 |
| PRIOR FILING DATE: 2003-01-10 |
| PRIOR PILING DATE: 2002-05-07 |
| PRIOR PILING DATE: 2002-05-07 |
| PRIOR PILING DATE: 2002-01-18 |
| PRIOR FILING DATE: 2002-01-18 |
| PRIOR PILING DATE: 2002-01-18 |
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Publication No. US2005049730A1

GENERAL INFORMATION:
APPLICANT: OGERSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR APPLICATION NUMBER: PCT/FR03/00178
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Sequence 63, Application US/11012353
Publication No. US20050249730A1
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ORGANISM: Homo sapiens
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APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DUFICOS, ALAIN

JAPPLICANT: HASUW, JEAN-FRANCOIS

APPLICANT: HEGER, OLIVIER

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT FILING DATE: 2003-12-16

PRIOR APPLICATION NUMBER: PR 0308538

PRIOR PILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: FR 0205753

PRIOR FILING DATE: 2002-05-07

PRIOR APPLICATION NUMBER: FR 020653

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.8%; Score 594; DB 7; Length 112; Best Local Similarity 99.1%; Pred. No. 3e-40; Matches 11; Conservative 1; Mismatches 0; Indels
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 67, Application US/11012353; Publication No. US20050249730A1; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-11-012-353-65
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US-11-012-353-67
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Best Local Similarity 91.1
Matches 102; Conservative
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Matches 101; Conservative
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Pred. No. 1.6e-36;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 91.9%; Score 547; DB 6; Length 112; Best Local Similarity 92.0%; Pred. No. 1.3e-36; Matches 103; Conservative 5; Mismatches 4; Indels
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| Sequence 26, Application US/10959310
| Publication No. US20050287138A1
| GENERAL INFORMATION: CR4-SPECIFIC AUTION:
| TITLE OF INVENTION: CR4-Specific antibody composition
| TITLE OF INVENTION: L249-363
| CURRENT APPLICATION NUMBER: US/10/959,310
| CURRENT FILING DATE: 2004-10-07
| PRIOR PILING DATE: 2003-10-08
| PRIOR FILING DATE: 2003-10-08
| PRIOR FILING DATE: 2004-10-08
| PRIOR FILING DATE: 2004-0-5-21
| NUMBER OF SEQ ID NOS: 46
| NUMBER OF SEQ ID NOS: 46
                                                                                                                                             TITLE OF INVENTION: CCR4-specific antibody composition;
FILE REFERENCE: 249-363
FILE REFERENCE: 249-363
CURRENT APPLICATION NUMBER: US/10/959,310
CURRENT FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: US 60/572,784
PRIOR PILING DATE: 2000-10-08
PRIOR PELING DATE: 2000-10-08
PRIOR PILING DATE: 2000-10-08
PRIOR PILING DATE: 2000-10-08
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 33
LENGTH: 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic peptide
                                                                               Sequence 33, Application US/10959310 Publication No. US20050287138A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

Best Local Similarity 91.1%;
Matches 102; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                                                                    US-10-959-310-33
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LENGTH: 112
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SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSLLPWTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                               APPLICANT: KYONA HAKKO KOGYO CO., LTD.
TITLE OF INVENTION: CCR4-specific antibody composition
FILE REFERENCE: 249-363
CURRENT APPLICATION NUMBER: US/10/959,310
CURRENT FILING DATE: 2004-10-07
FRIOR APPLICATION NUMBER: US 60/572,784
PRIOR FILING DATE: 2003-10-08
PRIOR FILING DATE: 2004-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATCHIN VEY. 2.1
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
TITLE OF INVENTION: CCR4-specific antibody composition
FILE REFERENCE: 249-363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 544; DB 6;
Pred. No. 2.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 543; DB 6;
Pred. No. 2.7e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.4%; Sco...
91.1%; Pred. No. c...
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/959,310
CURRENT FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: JP 2003-350162
PRIOR FILING DATE: 2003-10-08
PRIOR FILING DATE: 2004-10-08
PRIOR PLING DATE: 2004-0-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 34, Application US/10959310; Publication No. US20050287138A1; GENERAL INFORMATION:
                                                                                             US-10-959-310-35; sequence 35, Application US/10959310; Publication No. US20050287138A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: PRT
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Best Local
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                                                                                                                          Sequence 54, Application US/11012353
; Sequence 54, Application US/20050249730A1
; Sequence 54, Application No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: OCETSCH, LILIANE
; APPLICANT: COENCHIA, NATHALIE
; APPLICANT: COENCHIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: DUFLOS, ALAIN
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; TILLE REFERENCE: 01753-198
; CURRENT FILING DATE: 2004-12-16
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: FR 020553
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patentin Ver. 3.3
; SSO ID NO 5-4
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Publication No. US20050249730A1

GENERAL INPORMATION:
APPLICANT: GOEYGCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, ALAIN
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REPERENCE: 017733-198
CURRENT APPLICATION NUMBER: US/17612353
CURRENT PILLING DATE: 2004-12-16
PRIOR PILLOGATION NUMBER: 10/735,916
PRIOR PILLING DATE: 2003-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSLLPWTFGQGTKVEIK 112
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Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Mus musculus
US-11-012-353-54
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Sequence 56, Application US/11012353
; Boulication No. US20050249730A1
; GENERAL INFORMATION:
APPLICANT: GOETSCH. LILIANE
APPLICANT: CORVAIA. NATHALIE
APPLICANT: CORVAIA. NATHALIE
APPLICANT: CORVAIA. NATHALIE
APPLICANT: DUFLOS, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF
TITLE OF INVENTION: NOVEL 12-16
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT PRING DATE: 2003-12-16
FRIOR FILING DATE: 2003-12-16
FRIOR PLING DATE: 2003-07-11
FRIOR PLING DATE: 2003-07-11
FRIOR PLING DATE: 2003-07-07
FRIOR PLING DATE: 2003-06-07
FRIOR PLING DATE: 2002-06-07
FRIOR PLING DATE: 2002-01-08
FRIOR FILING DATE: 2002-01-18
FRIOR PLING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 122
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PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR PLING DATE: 2002-05-07
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 49
LENGTH: 122
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SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus US-11-012-353-49
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; ORGANISM: Mus musculus
US-11-012-353-56
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Matches 99; Conserv
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Query Match 87.4%
Best Local Similarity 86.6%
Matches 97; Conservative
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ORGANISM: Mus musculus
US-11-012-353-55
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| Publication No. US20550287148A1
| GENERAL INFORMATION:
| APPLICANT: Chatterjee, Malaya
| APPLICANT: Chatterjee, Sumil K.
| TITLE OF INVENTION: TREATMENT OF MELANOMA AND USE FOR THE
| TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
| TORRESPONDENCES: 66
| CORRESPONDENCES: ADDRESSE: ADDRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFQGGTKLEIK 131
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAECHLIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/089,266
FILING DATE: 23-Mar-2005
CLASSIFICATION DATA:
APPLICATION UNWBER: US/10/153,401
FILING DATE: 27-Mag-2002
APPLICATION NUMBER: US/10/153,401
FILING DATE: 1999-04-15
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lin, Rong-Hwa
APPLICANT: Chang, Chung Nan
APPLICANT: Chang, Chung Nan
APPLICANT: Chen, Pei-Jiun
APPLICANT: Chen, Pei-Jiun
APPLICANT: Huang, Chiu-Chen
TITLE OF INVENTION: ANTIBODIES
FILE REPERRENCE: 13062-011001
CURRENT FILING DATE: 2005-05-10
PRIOR APPLICATION NUMBER: US 60/569,892
PRIOR PILING DATE: 2004-05-10
NUMBER OF SEQ ID NOS: 100
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
TYPE: PRT
                                                                                                                                                                                                                                                                   ; Sequence 23, Application US/11125837; Publication No. US20050266003A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mus musculus
US-11-125-837-23
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                          RESULT 12
US-11-125-837-23
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Best Local S:
Matches 98
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Sequence 55, Application US/11012353
; Sequence 55, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
    APPLICANT: GORISCH, LILIANE
; APPLICANT: CORVAIA, NATHALIB
; APPLICANT: DUPLOS, ALAIN
; APPLICANT: DUPLOS, ALAIN
; APPLICANT: LEGER, OLIVIER
; APPLICANT: LEGER, OLIVIER
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; TITLE OF INVENTION: NOVEL 2014/1012, 353
; CURRENT APPLICATION NUMBER: 10/735, 916
; PRIOR APPLICATION NUMBER: PR 0308538
; PRIOR APPLICATION NUMBER: PR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR FILING DATE: 2003-07-11
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PR 0205753
; PRIOR APPLICATION NUMBER: PR 0205753
; PRIOR PILING DATE: 2002-05-07
; PRIOR PILING DATE: 2002-01-18
; PRIOR FILING DATE: 2002-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 522; DB 7;
Pred. No. 2.3e-34;
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
ATTORNEY/AGENT INFORMATION:
NAME: Catherine M. Polizzi
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
TELEPHONE: (415) 494-0792
TELEPHONE: (415) 494-0792
TELERA: 70614
INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acide
TYPE: amino acide
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SOFTWARE: PatentIn Ver. 3.3
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Matches 98; Conservative
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US-11-012-353-57
Sequence 57, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORINAL MITHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DEER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FRICK APPLICATION NUMBER: PR 02004-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: PR 0200654
PRIOR PRILICATION NUMBER: PR 0200654
PRIOR PRILICATION NUMBER: PR 0200654
PRIOR APPLICATION NUMBER: PR 0200654
PRIOR PRILING DATE: 2002-01-18
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DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                            1 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 60
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                                                                                                                                                                 Query Match 87.4%; Score 520; DB 7; Length 112; Best Local Similarity 86.6%; Pred. No. 1.6e-34; Matches 97; Conservative 10; Mismatches 5; Indels
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Search completed: January 10, 2006, 21:36:23 Job time : 6.71144 secs Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-735-916A-61

Sequence 61, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:

APPLICANT: GORISCH, Liliane

APPLICANT: GORISCH, Mathalie

APPLICANT: LEGER, Olivier

APPLICANT: BECK, Alain

APPLICANT: HAEUW, Jean-Francois

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 01753-183

CURRENT APPLICATION NUMBER: US/10/735,916A

FILE REFERENCE: 017753-183

CURRENT FILING DATE: 2003-12-16

FRIOR FILING DATE: 2003-07-11

FRIOR FILING DATE: 2003-01-20

FRIOR PILING DATE: 2003-01-18

FRIOR PILING DATE: 2002-01-18

FRIOR PILING DATE: 2002-01-18

FRIOR FILING DATE: 2002-05-07

FRIOR FILING DATE: 2002-05-07

FRIOR FILING DATE: 2002-05-07

FRIOR FILING DATE: 2002-05-07

FRIOR FILING DATE: 2002-01-18

FRIOR FILING DATE: 2002-05-07

FRIOR FILING DATE: 2002-05-07
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100.0%; Pred. No. 1.7e-46;
iive 0; Mismatches 0;
US-10-500-207A-43
US-10-500-207A-45
US-10-500-207A-45
US-10-201-452-14
US-09-94 T839-95
US-09-94 T839-95
US-10-201-452-13
US-10-301-301-30
US-10-505-980-20
US-09-73-436-66
US-10-745-115-66
US-10-745-115-66
US-10-745-115-66
US-10-482-105-38
US-10-482-105-39
US-10-482-105-39
US-10-482-105-31
US-10-482-105-31
US-10-482-105-31
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US-10-735-916A-63
; Sequence 63, Application US/10735916A
; Publication No. US20050084906A1
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Matches 112; Conservative
       ; ORGANISM: Homo sapiens
US-10-735-916A-61
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       SEQ ID NO 61
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                                 GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd
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US-10-735-916A-65

US-10-435-916A-182

US-10-431-469-19

US-10-434-469-19

US-10-258-728-28

US-10-500-207A-19

US-10-500-207A-19

US-10-258-728-27

US-10-258-728-27

US-10-258-728-27

US-10-434-469-41

US-10-438-105-39

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US-10-482-105-39

US-10-308-817-180

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Score

Result No.

9 9

Gaps

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; ORGANISM: Homo sapiens
US-10-735-916A-67
                                                               Query Match
Best Local Similarity
Matches 111; Conserv
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US-10-735-916A-65
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           GENERAL INFUGUATION:

GENERAL INFUGUATION:

APPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: DIEGER, Olivier

APPLICANT: BECK, Alain

APPLICANT: BECK, Alain

APPLICANT: HAEUW, Jean-Francois

ITILE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-183

CURRENT APPLICATION NUMBER: US/10/735,916A

CURRENT APPLICATION NUMBER: PG 303-07-11

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18
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APPLICANT: GORTSCH, Liliane
APPLICANT: CORVARA, Nathalie
APPLICANT: LEGER, Julian
APPLICANT: BUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVERTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
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100.0%; Score 595; DB 5; Length 131;
Best Local Similarity 100.0%; Pred. No. 2e-46;
Matches 112; Conservative 0; Mismatches 0; Indels 0
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CURRENT FILING DATE: 2003-12-16
PRIOR PULLING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2003-01-18
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR APPLICATION NUMBER: FR 02/05 654
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR SEQ ID NOS: 156
NUMBER OF SEQ ID NOS: 156
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Substitution US/10735916A
Publication No. US20050084906A1
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ORGANISM: Homo sapiens
US-10-735-916A-63
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ORGANISM: Homo sapiens
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20 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 79
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### PRINTEALION OF OSLOBERINGS |
### PRINTEAN: GORYAIA, Nathalie
#### APPLICANT: GORYAIA, Nathalie
#### APPLICANT: GORYAIA, Nathalie
#### APPLICANT: BEEK, Alain
#### APPLICANT: BEKK, Alain
### APPLICANT: BEKK, Alain
#### APPLICANT: BEKK, Alain
### APPLICANT: BEKK, Alain
### APPLICANT: BEKK, Alain
### APPLICANT: BEKK, Alain
### APPLICANT: WOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
### TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
### TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
### TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
### TITLE OF INVENTION: NUMBER: FR 03/08 538
### PRIOR APPLICATION NUMBER: PCT/FR 03/00 653
### PRIOR APPLICATION NUMBER: FR 02/00 653
### PRIOR APPLICATION NUMBER: FR 02/00 654
### PRIOR APPLICATION NUMBER: FR 02/00 654
### PRIOR APPLICATION NUMBER: FR 02/05 753
### PRIOR APPLICATION NUMBER: FR 02/05 753
### PRIOR APPLICATION NUMBER: PR 02/05 753
### PRIOR APPLICATION NUMBER: PR 02/05 753
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   Length 112;
                                                                         Indels
99.8%; Score 594; DB 5; Lilarity 99.1%; Pred. No. 2.1e-46; Conservative 1; Mismatches 0;
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Publication No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Rother, Russell
APPLICANT: WW, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT APPLICATION DATE:
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT APPLICATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 67, Application US/10735916A Publication No. US20050084906A1
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SEQ ID NO 67
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US-10-434-469-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Nobuo HANAI
APPLICANT: Motoo YAMASAKI
APPLICANT: AALKO FURUNA
APPLICANT: AALKO FURUNA
APPLICANT: Kenya SHITARA
APPLICANT: Kenya SHITARA
APPLICANT: Naoki SHIMADA
APPLICANTO: ANti-fiblroblast growth factor-8 monoclonal antibod
FILE REPERENCE: 249-310
CURRENT APPLICATION NUMBER: US/10/434,469
CURRENT PILING DATE: 2003-05-09
                                                                                                                                                                                                              1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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                                                                                                                                    Length 112;
                                                                                                                                  94.6%; Score 563; DB 4; Length 11
93.8%; Pred. No. 1.4e-43;
ive 4; Mismatches 3; Indels
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Pred. No. 1.4e-43;
4; Mismatches 3;
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TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 82 CIP (1087-37 CIP)
CURRENT APPLICATION NUMBER: US/10/453,698
CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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PRIOR FILING DATE: 1996-04-03
PRIOR PAPLICATION NUMBER: US 08/832,236
PRIOR FILING DATE: 1997-04-03
PRIOR FILING DATE: 1999-06-07
PRIOR FILING DATE: 1999-06-07
PRIOR APPLICATION NUMBER: US 09/876,040
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 182, Application US/10453698; Publication No. US20040038308A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/1043469
Publication No. US20040091480A1
GENERAL INFORMATION:
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93.8%;
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 93.8'
Matches 105; Conservative
                                                                                                                                    Query Match
Best Local Similarity 93.8
Matches 105; Conservative
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ORGANISM: human
                                                     ; TYPE: PRT
; ORGANISM: human
US-10-308-817-182
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US-10-453-698-182
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                    SEQ ID NO 182
LENGTH: 112
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Publication No. US20040253234A1

GENERAL INFORMATION:

APPLICANT: KYOWA HAKKO KOGYO CO., LTD

TITLE OF INVENTION: Humanized anti-FGF-8 antibody and the antibody fragment thereof

FILE REFERENCE: 11399WO1

CURRENT APPLICATION NUMBER: US/10/482,105

CURRENT FILING DATE: 2003-12-24

PRIOR PILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: VL synthetic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.6%; Score 563; DB 4; Length 112;
93.8%; Pred. No. 1.4e-43;
tive 5; Mismatches 2; Indels
                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 112
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Best Local Similarity 93.8%
Matches 105; Conservative
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US-10-258-728-28
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Best Local Similarity
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LENGTH: 112
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Publication No. US20050175608A1
GENERAL INFORMATION:
APPLICANT: KYOWA HAKKO KOGYO CO., LTD
TITLE OF INVENTION: AGENT FOR TREATING ARTHRITIS
FILE REFERENCE: 1442
CURRENT APPLICATION NUMBER: US/10/500,207A
CURRENT FILING DATE: 2004-06-28
PRIOR PILING DATE: 2001-12-28
NUMBER OF SEQ ID NOS: 51
SOFTWARE PATCHTIN Version 3.1
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Publication No. US20050175608A1
GENERAL INFORMATION:
APPLICANT: KYOWA HAKKO KOGYO CO., LTD
TITLE OF INVENTION: AGENT FOR TREATING ARTHRITIS
FILE REFERENCE: 1442
CURRENT APPLICATION NUMBER: US/10/500,207A
CURRENT APPLICATION NUMBER: JP2001-400677
PRIOR FILING DATE: 2001-12-28
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SOFWARR: Patentin version 3.1
SEQ ID NO 19
LENGTH: 112
                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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  SOFTWARE: Patentin Ver.
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US-10-500-207A-19
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                      SEQ ID NO 17
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APPLICANT: Blis, John Robert Maxwell
APPLICANT: Durant, Linda Gillian
TITLE OF INVENTION: Humanised Antibodies to the Epidermal Growth Factor Receptor
TITLE OF INVENTION: Humanised Antibodies to the Epidermal Growth Factor Receptor
TITLE OF INVENTION: 2013-610801
CURRENT APPLICATION NUMBER: 2003-6-18
PRIOR APPLICATION NUMBER: GB 0011981.8
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                                                                                        OTHER INFORMATION: LV.2-2, a designed amino acid sequence of VL of OTHER INFORMATION: an anti-FGF-8 CDR-grafted neutralizing antibody
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Sequence 6, Application US/10388214A

Publication No. US20040082762A1

GENERAL INFORMATION:

APPLICANT: Basi, Guriq

APPLICANT: Basi, Guriq

APPLICANT: Baldanha, Jose

ITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA

ITLE OF INVENTION: AMYLOID PEPTIDE

FILE REFERENCE: ELN-004

CURRENT APPLICATION NUMBER: US/10/388,214A

CURRENT FILING DATE: 2003-03-12

PRIOR APPLICATION NUMBER: US 60/363,751

PRIOR FILING DATE: 2002-03-12

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                    94.1%; Score 560; DB 5; Length 112; 93.8%; Pred. No. 2.6e-43; ive 5; Mismatches 2; Indels
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TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-500-207A-47
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US-10-258-728-27
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Sequence 26, Application No. US20040091485A1

GENERAL INFORMATION:

APPLICANT: Blis, John Robert Maxwell

APPLICANT: Durrant, Linda Gillian

ITILE OF INVENTION: Humanised Antibodies to the Epidermal Growth Factor Receptor

FILE REFERENCE: 28438-101US01

CURRENT APPLICATION NUMBER: US/10/258,728

CURRENT APPLICATION NUMBER: GB 0011981.8

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-06-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.1

SEQ ID NO 26

LENGTH: 112
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APPLICANT: Akiko FURUYA
APPLICANT: Akira TANAKA
APPLICANT: Kenya SHITARA
APPLICANT: Kenya SHITARA
APPLICANT: Mooki SHITARA
ITILE OF INVENTION: Anti-fiblroblast growth factor-8 monoclonal antibod
FILE REFERENCE: 249-310
                                                                                                                                                                                                                                                                                           0; Gaps
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Pred. No. 3.2e-43;
3; Mismatches 5
                         GB 0020794.4
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Publication No. US20040091480A1
GENERAL INFORMATION:
APPLICANT: Nobuo HANAI
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: GB 002;
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 27
LENGTH: 112
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92.9%;
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Best Local Similarity 92.94
Matches 104; Conservative
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Matches 104; Conservative
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CRGANISM: Mus musculus
US-10-258-728-27
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US-10-434-469-41
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OTHER INFORMATION: Description of Artificial Sequence: LV.3-1 of VL of KM8036
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CURRENT APPLICATION NUMBER: US/10/434,469
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: UP 08-081754
PRIOR FILING DATE: 1996-04-03
PRIOR FILING DATE: 1997-044-03
PRIOR PILING DATE: 1997-044-03
PRIOR FILING DATE: 1997-04-03
PRIOR FILING DATE: 1997-04-07
PRIOR FILING DATE: 1999-06-07
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 41.0
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ORGANISM: Artificial Sequence
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USA
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                                                              January 10, 2006, 20:34:27; Search time 21.8706 Seconds (without alignments) 423.384 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6_COMB.pep:*

(cgn2_6/ptodata/1/iaa/H_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-331-398A-50
US-08-331-397B-50
US-08-31-397B-50
US-09-227-693-50
US-08-053-171-15
US-08-015-190A-14
US-08-129-930B-95
US-08-97-288A-95
US-08-98-66
US-08-482-882-66
US-08-483-389-66
US-08-483-389-66
US-08-483-389-66
US-08-483-389-66
US-08-483-389-66
US-08-483-389-66
US-08-483-932-66
US-08-473-503-66
US-08-473-503-66
US-08-473-503-66
US-08-473-503-66
US-08-473-503-66
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5-09-192-838B-2
5-09-324-191-2
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                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-331-397B-48
US-08-759-804A-48
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                                                                                                                                                                                        572060 segs, 82675679 residues
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                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          protein search, using sw model
                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                    seq length: 0
seq length: 200000000
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          Copyright
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                                                                                                                       Perfect score:
                                                                                                                                                                                                                                    Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                   Sequence:
                                                                                                                                                                                         Searched:
                                                                Run on:
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        28
        520
        87.4
        112
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        US-09-002-753A-3
        Sequence 3, Appliance 3, Ap
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ALIGNMENTS

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Gaps

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1 DVLMTQSPLSLPVTPGEPASISCRSSQIIVHSNGNTYLEWYLQKPQQSPQLLIXKVSNRF 60
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Score 560; DB 1; Length 112;
Pred. No. 1.8e-47;
3; Mismatches 3; Indels
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US-08-759-804A-50
US-08-759-804A-50

| Sequence 50, Application US/08759804A
| Patent No. 5990266
| GENERAL INFORMATION:
| APPLICANT: Platean, Ira
| APPLICANT: FitzGerald, David J.
| TITLE OF INVENTION: Fusion Proteins, and Uses Thereof NUMBER OF SEQUENCES: 68
| CORRESPONDENCE ADDRESS: 68
| CORRESPONDENCE ADDRESS: 7
| ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CENTY: CONTRACT CONTRACT CENTY CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Humanized B3 Variable Light chain (V-L) (HumB3V-L)"
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

CLASSIFICATION:

APPLICATION NUMBER:

BIONR APPLICATION DATA:

APPLICATION NUMBER:

PILING DATE:

APPLICATION NUMBER:

PILING DATE:

APPLICATION NUMBER:

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGIESTRATION UNDHER: 32,762
REFRENCE/DOCKET NUDBER: 0152;
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
Query Match

Best Local Similarity 94.6%;
Matches 106; Conservative 3
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amino acid
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OTHER INFORMATION:
OTHER INFORMATION:
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APPLICANT: Benhar, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRES:
ADDRESSE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTVLQWYLQKPGQSPQLLIXKVSNRL 60
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                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                Length 112;
                                            LOCATION: 1..112

TOTHER INFORMATION: /note= "Humanized B3 Variable Light;

OTHER INFORMATION: chain (V-L) (HumB3V-L)"
US-08-331-398A-50
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chain (V-L) (HumB3V-L)"
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ZIP: 94105-1492

COMPUTER READABLE FORM:
MEDIUW TYER: E-PLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/767,331
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: HULLEY. TOM
                                                                                                                                                                                                                                                       Score 560; DB 1;
Pred. No. 1.8e-47;
3; Mismatches 3;
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; Sequence 50, Application US/08331397B
Patent No. 5981726
; GENERAL INFORMATION:
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REGISTRATION NUMBER: 38,498
REPRENCE/DOCKET NUMBER: 01528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-9600
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 anino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 94.6%;
Matches 106; Conservative
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MOLECULE TYPE: protein
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; OTHER INFORMATION:
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US-08-331-397B-50
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        NAME/KEY:
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1 DVIAMIQSPLSLPVTPGEPASISCRSSQIIVHSNGNTYLEWYLQKPGQSPQLLIXKVSNRF 60
1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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OTHER INFORMATION: /note= "Residue that has been
OTHER INFORMATION: replaced with mouse amino acid in the humanized
                                                                                                                                                                        61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPFTFGQGTKVEIX 112
                                                                                                                                 61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Complementarity-determining
region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Complementarity-determining
                                                                                                                                                                                                                                                                                                                                   US-08-053-171-15
Sequence 15, Application US/08053171
Sequence 15, Application US/08053171
Sequence 15, Application US/08053171
SERENAL INFORMATION:
APPLICANT: Co, Loibner
TITLE OF INVENTION: Antibody Derivatives
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
STREET: 379 Lytton Avenue
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/053,171

FILING DATE: 22-APR-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: SMITH, Willaim REGISTRATION NUMBER: 30,223

REFRENCE/DOCKET NUMBER: 30,223

REFRENCE/DOCKET NUMBER: 11823-54-1

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 15: 586-2400

INFORMATION FOR SEQ ID NO: 15: 586-2600

INFORMATION FOR SEQ ID NO: 15: 586-2600

IRROGHNER CHRRACTERISTICS:

LENGTH: 112 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: Region
LOCATION: 24..39
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
Patent No. 5562903
OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
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NAME/KEY: Region
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LOCATION: 94..10
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                                                                                                            1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 50, Application US/09227693
Sequence 50, Application US/09227693
Patent No. 6287562
GENERAL INFORMATION:
APPLICANT: PASTAN, Irai
APPLICANT: BENHAR, Itai
APPLICANT: PADLAN, Eduardo A.
APPLICANT: JUNG, Sun-Hee
APPL
                                                                                                                                                                                                                                           61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCRQGSHVPFTFGQGTKVEIK 112
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                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1..112
OTHER INFORMATION: /note= "Humanized B3 VL region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend Khourie and Crew STRRET: Steuart Street Tower, One Market Plaza CITY: San Prancisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94105-1493

ZIP: 94105-1493

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
   94.6%; Pred. No. 1.8e-47; ive 3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 13,762
REFERENCE/DOCKET NUMBER: 15280-126-1-3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 112 amino acids
   Best Local Similarity 94.6
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Protein
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Query Match
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                                                                                                                                                                                                                                                                                                                               1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPQLLISKVSNRF 60
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                                                                                                                                                                                                                                               Gaps
                                                                                     /note= "Residue in the framework that is replaced with mouse amino acid in the humanized antibody."
                                                                                                                                                                                                                                                                                                                                                                                                       61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPGGSHVPFTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08815190A

Facture No. 6046310

GENERAL INFORMATION:
APPLICANT: Queen, Cary L.
APPLICANT: Schneider, William P.
APPLICANT: Schneider, William P.
APPLICANT: Pasquez, Maximiliano
TITLE OF INVENTION: Fas Ligand Fusion Proteins and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 17
CORRESPONDENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Prancisco
STRIES California
COUNTRY: USA
                                                                                                                                                                                                   Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "mature light chain variable region of humanized ABL 364 antibody"
                                                                                                                                                                                                                                        3; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,190A
                                                                                                                                                                                              93.4%; Score 556; DB 1;
93.8%; Pred. No. 4.4e-47;
iive 4; Mismatches 3
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FILING DATE: 11-MAR-1997
CLASSIFICATION 536
FILING APPLICATION 536
FRIOR APPLICATION DATE: US 08/614,584
FILING DATE: 13-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPLE, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 011823-006710US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
  OTHER INFORMATION: antibody."
                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                   Best Local Similarity 93.8
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
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; OTHER INFORMATION:
; OS-815-190A-14
                                                                                  OTHER INFORMATION:
OTHER INFORMATION:
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                       FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                     US-08-053-171-15
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                                                                                                                      1 DIVWIQSPLSLPVIPGEPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPQLLISKVSNRF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DVVMTQSPLSLPVTPGBPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                    Gaps
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                                                                                                                                                                                    61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                              61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPFTFGQGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                Sequence 95, Application US/08129930B
; Sequence 95, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
    APPLICANT: do Couto Dr., Pernando J.R.
    APPLICANT: Ceriani Dr., Roberto L.
    APPLICANT: Padlan Dr., Bourardo A.
    APPLICANT: Padlan Dr., Banardo A.
    APPLICANT: Padlan Dr., Banardo A.
    APPLICANT: Padlan Dr., Banardo A.
    APPLICANT: Padlan Dr., Carcinoma Specificity, and Kit and TITLE OF INVENTION: Diagnostic Vaccination and TITLE OF INVENTION: Diagnostic Wethods
    NUMBER OF SEQUENCES: 96
Score 556; DB 2; Length 112;
Pred. No. 4.4e-47;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2055 No. 5804187th Broadway, Suite 201 CITY: Walnut Creek STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER, TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERALING SYSTEM: FC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: September 30, 1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 544; DB 1;
Pred. No. 7.7e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRE
TELECOMMUNICATION INFORMATION:
    93.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: n.a.
INFORMATION FOR SEQ ID NO: 95:
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91.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : (510) 521-1333
(510) 521-3541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 131 amino acids TYPE: amino acid
                                                 Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-08-129-930B-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: V. AMZEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                            Similarity
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Best Local Simil
Matches 102; C
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                              Best Local
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APPLICATION NUMBER: US/08/482,882
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.4%;
91.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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amino acid
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Best Local Similarity 91.1'
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: n.a.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
Los Angeles
: California
XY: USA
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-08-976-288A-95
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                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                  APPLICANT: do Couto, F.J.R.
APPLICANT: Ceriani, R.L.C.
APPLICANT: Petersen, J.A.
TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: do Couto Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Pedalan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Pretty, Schroeder & Poplawski
STRREET: 444 South Flower St., 19th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10022-7499
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,346A
FILING DATE: 08-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
91.4%; Score 544; DB 2;
Best Local Similarity 91.1%; Pred. No. 7.7e-46;
Matches 102; Conservative 6; Mismatches 4;
                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEB: Ostrager, Chong & Flaherty
STREET: 300 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLT 149,608
              Sequence 50, Application US/08134346A Patent No. 6281335 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 95, Application US/08976288A Patent No. 6315997
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY, AGENT INFORMATION:
NAME: ONOFILO, Dara L.
REFERENCE/DOCKET NUMBER: 34,889
REFERENCE/DOCKET NUMBER: CLT
TELECOMMUNICATION INFORMATION:
TELERPHONE: 212-826-6565
TELEFAX: 212-826-5509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 131 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                     New York
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  US-08-134-346A-50
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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20 DVLMTQTPLSLPVTPGEPASISCRSSQSIVHSNGNTYLEMYLQKPGQSPQLLIYKVSIRF 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 7.7e-46;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 66, Application US/08482882
Patent No. 577318
GENERAL THORMATION
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,696
FILING DATE: No. 6315997ember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel Ph.D.
REGISTRATION NUMBER: 30, 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSOSTHVPYTFGQGTKVEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 66, Application US/08483389

Patent No. 5811517
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITILE OF INVENTION: ICAM-RELATED PROTEIN
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: Olited States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.3%; Score 543; DB 1; Length 116; 91.1%; Pred. No. 8.5e-46; Live 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWREN: PAPELICATION DATA:
APPLICATION NUMBER: US/08/483,389
FILING DATE: 07-001-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 33.02
ATTORNEY/AGENT INPORMATION:
NAME: No. 5773218and, Greta E.
REGISTRATION NUMBER: 35,302
TELEFRAX: (312) 474-6300
TELEFRAX: (312) 474-6448

ITELEFRAX: 25-386
INPORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TTYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 91.1
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-08-482-882-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-08-483-389-66
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1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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; Sequence 66, Application US/08487113D
; Patent No. 583782.
; GENERAL INFORMATION:
    APPLICANT: Gallatin, W. Michael
    APPLICANT: Vazeux, Rosemay
    TITLE OF INVENTION: ICAM-Related Materials and Methods
    NUMBER OF SEQUENCES: 120
    CORRESPONDENCE ADDRESS:
    ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
    CITY: Chicago
    STATE: Illinois
    COUNTRY: United States of America
    ZIP: 6060-6402
    COMPUTER: READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFFWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION NUMBER: US/08/487,113D
    FILING DATE:
    CLASS PETALES.
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               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 20-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY FAGENT INPORMATION:
NAME: SUL, YOUNG J.
REGISTRATION NUMBER: P-41,337
REGISTRATION NUMBER: P-41,337
RECISCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION NUMBER: US 08/102,852
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 66:
FILING DATE: 05-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 116 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-389-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sest Local Similarity
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Query Match
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Patent No. 5869262

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
TORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Galo Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 91.3%; Score 543; DB 1; Length 116; Best Local Similarity 91.1%; Pred. No. 8.5e-46; Matches 102; Conservative 5; Mismatches 5; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,503
FILING DATE: 07-UMN-1995
CLASSIFICATION 3435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO -5837822and/Greta E.
REGISTRATION NUMBER: 35,302
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECO
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-08-487-113D-66
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5 DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRF 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPYTFGQGTKVEIK 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.3%; Score 543; DB 1; Length 116; 91.1%; Pred. No. 8.5e-46; Live 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 66, Application US/08483932
Patent No. 5880268
GENERAL INFORMATION:
APPLICANT: Vacalatin, W. Michael
APPLICANT: Vacaux, Rosemay
ITILE OF INVENTION: ICAM-Related Materials and Methods
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,932
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
PRICR APPLICATION DATA:

APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-UN-1992
PRICR APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRICR APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5869265and, Greta E.
REGIERROEF/OCCKET NUMBER: 35.302
REFERENCE/OCCKET NUMBER: 32178
FELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-UAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 116 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 91.1
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-473-503-66
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STREET: 6000
CITY: Chicago
STATE: Illinois
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US-08-483-932-66
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| Sequence 66, Application US/08720420A |
| Sequence 66, Application US/08720420A |
| Patent No. 5989843 |
| Patent No. 5989843 |
| APPLICANT: Gallatin, W. Michael |
| APPLICANT: Gallatin, W. Michael |
| APPLICANT: Vazeux, Rosemay |
| TITLE OF INVENTION: ICAM-Related Materials and Methods |
| UNMBER OF SEQUENCES: 120 |
| CORRESSED Marshall, O'Toole, Gerstein, Murray & Borun STREET: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Chicago |
| STREET: Marshall, O'Toole, Gerstein, Murray & CUTY: Chicago |
| STREET: Marshall, O'Toole, Gerstein, Murray & Borun STREET: United States of America |
| COWNTRY: United States of America |
| COMPUTER READABLE FORM: |
| MEDIUM TYPE: Floppy disk |
| COMPUTER: IBM PC compatible |
| OPERATING SYSTEM: PC-DOS/MS-DOS |
| SOFTWARE: Patentin Release #1.0, Version #1.25 |
| CURRENT APPLICATION DATA: |
| APPLICATION DATA: |
| APPLICATION DATA: |
| CURRENT APPLICATION DATA: |
| CURRENT APPLICATION DATA: |
| COMPUTER: PLANT APPLICATION DATA: |
| COMPUTER: PLA
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91.3%; Score 543; DB 1; Length 116
Best Local Similarity 91.1%; Pred. No. 8.5e-46;
Matches 102; Conservative 5; Mismatches 5; Indels
APPLICATION NUMBER: US U7/027, CL
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889, 724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827, 689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
FELENCHOMEN: 33102
REFERENCE/DOCKET NUMBER: 33178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6340
TELEPHONE: (312) 474-6448
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TOPOLOGY: linear
MOLECTLE TYPE: protein
US-08-483-932-66
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING APPLICATION DATA:
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| PRIOR APPLICATION DATA:
| PRIOR APPLICATION DATA:
| APPLICATION NUMBER: US 07/894,061
| FILING DATE: 05-UNA: 1992
| FILING DATE: 05-UNA: 1992
| PRIOR APPLICATION NUMBER: US 07/889,724
| FILING DATE: 26-MAY: 1992
| PRIOR APPLICATION NUMBER: US 07/827,689
| PRIOR APPLICATION NUMBER: US 07/827,689
| PRIOR APPLICATION NUMBER: 36.659
| ATTORNEY/AGENT INPORMATION: PREJECTATION NUMBER: 33.659
| ATTORNEY/AGENT INPORMATION: PREJECTATION NUMBER: 33.659
| PRIOR PRIOR PRIOR PRIOR NUMBER: 33.659
| PRIOR PRIOR PRIOR PRIOR NUMBER: 33.659
| PRIOR PRIOR PRIOR PRIOR PRIOR NUMBER: 33.699
| PRIOR PRIOR PRIOR PRIOR PRIOR NUMBER: 33.699
| PRIOR PRI
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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OM protein - protein search, using sw model

January 10, 2006, 20:28:02; Search time 13.5124 Seconds (without alignments) 797.508 Million cell updates/sec Run on:

1 DVVMTQSPLSLPVTPGEPAS......CFQGSHVPWTFGQGTKVEIK 112 US-10-735-916A-61 Perfect score: Sequence:

283416 seqs, 96216763 residues Gapop 10.0 , Gapext 0.5 Searched:

BLOSUM62

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		-		chain		_	-	chain		chain	chain		chain	chain	chain pr	chain V	chain V	chain	chain V-	chain		chain		chain	chain	chain pr	chain pr		chain V
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i	B39276	PL0203	S52028	A31807	PC4203	826335	S58207	838719	840357	A32967	PT0359	B34904	B31485	C27887	C34904	A27887	F27887	838715	B3296.	E27887	B30577	S26882	K2HURP	S16112		D34904	B32513	0	D2819
DB	~	~	N	N	7	7	7	N						~															
% Query Match Length	131	113	219	112	219	110	112	112	136	114	118	131	112	112	131	112	112	115	114	112	131	132	133	219	103	131	131	135	112
% Query Match	1 00	7	86.9	86.4	86.4	9	ė.	86.2	86.2	85.7	85.5	85.5		84.9	84.9	84.5	84.4	84.4	84.2	84.0	84.0	84.0	84.0	84.0		83.9	83.9	83.9	83.7
8	524	523	517	514	514	513	513	513	513	510	509	509	507	505	505	503	502	502	501	200	200	200	200	200	499	499	499	499	498
Result No.	1	8	ю	4	S	9	7	80	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59

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117	112	225 126 142	133 131 133	112 125 131
83.7	83.2 83.2 83.2	83.0 82.9	82.7 82.5 82.5	82.4 82.4 82.4
498 497	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	494 493.5 493	492 491 491	4 9 0 4 9 0 4 9 0
30	2 6 8 8 2 6 4 8	36 38 38	4 4 4 2 1 1 0	4 4 4 4 4 5 5

ALIGNMENTS

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		recontract
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7 1706	9276	1400

A;Cross-references: UNIPARC:UP10000115153; GB:M55313; NID:g198095; PIDN:AAA63385.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: immunoglobulin F; 35-114/Domain: immunoglobulin homology < IMM>

ö Gaps .. 0 88.1%; Score 524; DB 2; Length 131; 87.5%; Pred. No. 1.6e-42; Attive 9; Mismatches 5; Indels 98; Conservative Query Match Best Local Similarity Matches 98; Conserv

1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60 20 DVLATQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 79 셤 ò

61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPWTFGQGTKVEIK 112 80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGSGTKLEIK 131 ઠે g

arni-DNA autoantibody BV17-31, kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: PLO203
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from 1 A;Reference number: PLO198; MUID:90309768; PMID:2114528
A;Reference complement: PLO303
A;Molecule type: mRNA
A;Residues: 1-113 <SMIA
A;Cross-references: UNIPARC:UPI0000113786; GB:X53643; NID:g50196; PIDN:CAA37694.1; PID::C;Superfamily: immunoglobulin homology <IVM'>F;16-95/Domain: immunoglobulin homology <IVM'>F;16-95/Domain: immunoglobulin homology <IVM'>F;16-95/Domain: immunoglobulin homology <IVM'>F;16-95/Domain: complementarity-determining 3
F;34-102/Region: complementarity-determining 3
F;101-113/Region: D region

us-10-735-916a-61.rpr

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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C;Datesion: PG4203
R;Kwak, J W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mc A;Reference number: PC4202; MUID:97082978; PMID:8964510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: mRNA

A,Rebidues: 1-219, cKMA-

A,Gross-references: UNIPARC:UPI00001157E4; GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID.

C,Comment: This protein is specific for human plasma apolipoprotein A-I of high-density

C,Superfeaulty: immunoglobulin V region; immunoglobulin homology

F;1-112/Domain: V region #status predicted <RRG>

F;113-219/Domain: C region #status predicted <CRG>
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C,Accession: S26335
J, Sklark, S.B.; Caton, A.J.
J, Exp. Med. 174, 613-624, 1991
A,Title: Antibodies that are specific for a single amino acid interchange in a protein e. A,Reference number: S26309; MUID:91341421; PMID:1908510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UP10000115F78; EMBL:X59183; NID:g52314; PIDN:CAA41893.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology <IMM>
F;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHTNGNTYLEWYLQKPGQSPKLLIYKVSNRF 60
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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                                   61 SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWOGSHVPYTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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Pred. No. 1.4e-41;
9; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 219;
                                                                                                                                                                                                                                      Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 514; DB 2;
Pred. No. 2.5e-41;
9; Mismatches 6;
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86.6%;
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Best Local Similarity 87.34
Matches 96; Conservative
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Best Local Similarity 80...
2 97; Conservative
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A;Molecule type: mRNA
A;Residues: 1-110 <STA>
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A31807

Ig kappa chain V region (PAC1) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 20-Jul-1989 #sequence_revision 20-Jul-1989 #text_change 09-Jul-2004
C;Accession: A31807
R;Taub, R.; Gould, R.J; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shatt
J. Biol. Chem. 264, 259-265, 1989
A;Title: A monocolonal antibody against the platelet fibrinogen receptor contains a seque
A;Reference number: A31807
A;Accession: A31807
A;Accession: A31807
A;Accession: A31807
A;Residues: 1-112 <TAU>
A;Residues: 1-112 <TAU>
C;Superfemily: immunoglobulin V region; immunoglobulin homology
C;Superfemily: immunoglobulin homology <!NM>
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                                                                                                                                                                                                             DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF
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                                                                                                                                                                                                                                                                                                         61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                             SGVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPFTFGSGTKLBIK 112
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                                   Length 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 517; DB 2; Length 21
Pred. No. 1.3e-41;
6; Mismatches 7; Indels
                                                                                                   Indels
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                            ; DB 2;
1.7e-42;
                            ch 87.9%; Score 523; DB Similarity 87.5%; Pred. No. 1.7e 98; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.4%;
Matches 99; Conservative
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Best Local Similarity
Matches 96; Conserv
                                                               Best Local Similarity
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Ig kappa chain - mouse
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A;Cross-references: UNIPROT:QBNEKO; UNIPARC:UPI0000176CA8; EMBL:X72467 C;Superfamily: immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;36-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.9%
Matches 94; Conservative
                                                                                                                                                              Best Local Similarity 86.6
Matches 97; Conservative
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A; Residues: 1-118 <SHE>
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  C; Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000
C; Accession: S58207
R; Melschof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, submitted to the EMBL Data Library, July 1995
A; Description: Characterization of heavy and light chain immunoglobulin variable region A; Accession: S58206
A; Accession: S58207
A; Accession: Dreliminary
A; Status: preliminary
A; Relevance usuber: MELA
A; Residues: 1-112 < wELA
A; Residues: 1-112 < wELA
A; Cross-references: UNIPARC: UPI0000116253; EMBL: X89056; NID: 9929642; PIDN: CAA61443.1; PI
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S38719
R; Cimanis, A.Y.
Submitted to the EMBL Data Library, November 1993
A; Reference number: S38713
A; Accession: S38719
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-12 < CIM>A; Residues: 1-12 < CIM>A; Cross-references: UNIPARC: UPI0000117543; EMBL: X76021; NID: 9416112; PIDN: CAA53608.1; S; Superfamily: immunoglobulin V region; immunoglobulin homology
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C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C;Accession: S40357
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3371, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig light chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: 338719
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85.7%; Pred. No. 1.5e-41;
ive 10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Length 112;
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Pred. No. 1.5e-41;
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A,Status: preliminary, translation not shown A,Molecule type: mRNA
A,Residues: 1-136 < KLE>
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Best Local Similarity 86.6%;
Matches 97; Conservative
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Matches 96; Conservative
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Ig kappa chain V-II region TE33 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 21-Jan-2000
C;Accession: A32967
R;Levy, R.; Assulin, O.; Scherf, T.; Levitt, M.; Anglister, J.
Biochemistry 28, 7168-7175, 1989
A;Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, pred1 A;Reference number: A32967; MUID:90057406; PMID:2819059
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A;Molecule type: mRNA
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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
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                                                                     Gaps
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R,Shefner, R.; Kleiner, G.; Turken, A.; Papazian, L.; Diamond, B.
R,Shefner, R.; Xleiner, G.; Turken, A.; Papazian, L.; Diamond, B.
A,Title: A novel class of anti-DNA antibodies identified in BALB/c mice.
A,Reference number: PT0352; MUID:91108325; PMID:1988536
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85.5%; Score 509; DB 2; Length 118;
Best Local Similarity 84.8%; Pred. No. 3.7e-41;
Matches 95; Conservative 9; Mismatches 8; Indels
   Length 136;
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C;Comment: This protein is an anti-double-stranded DNA antibody.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;19-98/Domain: immunoglobulin homology <IMM>
                                                                 Indels
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86.2%; Score 513; DB 2; L
86.6%; Pred. No. 1.8e-41;
ive 3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V region (R4A.12) - mouse (fragment)
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C;Accession: C27887
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
A;Title: Structural and functional implications of a restricted antibody response to a d
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: C27887
                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-112 <CAT>
A;Cross-references: UNIPARC: UNIPARC: UPI0000176A17
A;Expenental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-res A;Reference number: A34903; WUID:90094387; PMID:2104617
A;Accession: C34904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Stacus: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-131 - ABD.
A;Residues: 1-131 - ABD.
A;Cross-references: UNIPROT: QBVCI6; UNIPARC: UDI00001767A8
B;Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
A;Dil. Chem. 264, 1565-1569, 1989
A;Title: Comparison of variable region primary structures within an anti-fluorescein idi
A;Reference number: A31485; MUID:89109167; PMID:2492278
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C:Species: Wus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
C:Accession: C34904; I31485
                                                       Ig kappa chain V region (H37-82) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQRPGQSPELLIYKVSNRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQRTHVPWTFGGGTKLEIK 112
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83.9%; Pred. No. 9.9e-41;
ive 9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;16-95/Domain: immunoglobulin homology <IMM>
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A;Residues: 20-52 <BE2>
A;Cross-references: UNIPARC:UP100001767A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94; Conservative
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                                                                                                                                                                                                                                                                          RESULT 12
B34904
IQ Kappa chain precursor V region (12-40 and 5-14) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C;Accesion: B34904, #134903
R;Bedzyk, W.D.; Herron, J.M.; Edmundson, A.B.; Voss Jr., E.W.
J; Biol. Chem. 265, 133-138, 1990
A;Tible. Active site structure and antigen binding properties of idiotypically cross-rea A;Reference number: A34904
A;Reference number: A34904
A;Reference number: A34904
A;Rocession: B34904
A;Rocession: B34904
A;Rocession: B34904
A;Rocession: B34904
A;Rocession: B34904
A;Rocession: B34904
C;Residues: 1-131 ABBD
A;Cross-references: UNIPARC:UPI0000114FC8; GB:M32384; GB:J05237; GB:J05238; NID:g639656; C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heteroterramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
B31485
Ig kappa chain V region (4-4-20) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 09-Jul-2004
R;Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J;December of variable region primary structures within an anti-fluorescein idia
A;Reference number: A31485
A;Reterence number: A31485
A;Rocession: B31485
A;Rocession: B31485
A;Rocession: B31485
A;Rocession: B31485
A;Rocession: immunoglobulin an immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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9
                                                           63
                                    DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRP
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                                                                                                                                                          SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPWTFGGGTKLEIK 115
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                                                                                                                            YGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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Pred. No. 4.1e-41;
9; Mismatches 8; Indels
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Best Local Similarity 84.8%;
Matches 95; Conservative
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nes 94; Conserv
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Best Local S:
Matches 94
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P18135 P Q9u178 P P01653 P P01653 P P01667 n P01657 n P01627 P P01660 n P01660 n P01664 P P01668 n P01668 n P01668 n

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homo sapien homo sapien homo sapien mus musculu

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DVLMTQSPLSLPVSLGDQASISCRSSQIIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 195
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NUCLECTION SEQUENCE.

NUCLESCIOS SEGUENCE.

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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.4%; Score 520; DB 2; Length 24
87.5%; Pred. No. 5.5e-46;
ive 8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 AA; 26634 MW; 7A3759B43E570950 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KY2F HUMAN STANDARD; PRT; 133 AA. P06310; 01-37N-1988 (Rel. 06, Created) 01-37N-1988 (Rel. 06, Last sequence update) 01-3N-2005 (Rel. 47, Last annotation update) 1g kappa chain V-II region RPMI 6410 precursor. Homo sapiens (Human).
                                  KV3E HŪMAN
KV3E MOUSE
KV2B MOUSE
KV2B MOUSE
KV3A HUMAN
GOFILE HUMAN
KV3H HÜMAN
KV3F HUMAN
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25-0CT-2004 (TEMBLEEL 28,
25-0CT-2004 (TEMBLEEL 28,
25-0CT-2004 (TEMBLEEL 28,
B3 (FV) - PE40 (TEMBLEEL 28,
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1046.577 Million cell updates/sec
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P01617
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Q5f210
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                              2166443 seqs, 705528306 residues
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                                                                                                                                 January 10, 2006, 20:26:41;
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KV4C HUMAN
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Maximum Match 100%
Listing first 45 summaries
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KV3B_HUMAN
KV3D_HUMAN
                                                                                               protein search, using sw model
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2: uniprot_trembl:*
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Database :

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
Klobeck H.G., Solomon A., Zachau H.G.; "Contribution of human V kappa II germ-line genes to light-chain
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003596; Ig_v.
SWART; SW00406; IGv; 1.
PROSITE: S0815; IG_LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                          EMBL, Z00009; -; NOT ANNOTATED_CDS; Genomic_DNA. PIR; A01889; KZHUGM. HSSP; Q99M7; 1191.
SMR; P063109; 5-117.
GO; GO:0005576; C:extracellular region; NAS. GO; GO:0005823; F:amtigen binding; NAS. InterPro; IPR007110; Ig-like.
                                                                Nature 309:73-76(1984).
                                           diversity.
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01-JAN'1988 (Rel. 06, Last sequence update)
01-JAN'1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-II region GM607 precursor (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Burchontoglires; Primates; Catarrhini; Hominidae;
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                              NUCLEOTIDE SEQUENCE.
MEDLINE=86041852; PubMed=2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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84.8%; Pred. No. 3.3e-44;
ive 8; Mismatches 9; Indels
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Framework-3.
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PR; A01890; KZHURP.
HSSP, Q99M37; 1191.
SMR; P06310; 21-133.
                                                                                                                                                                                                                            Nucleic Acids Res. 13:6499-6513(1985)
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PROSITE; PS50835; IG LIKE; 1
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nes 95; Conservative
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01-JAN-1988 (
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Homo sapiens (Human).
Eukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                 1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                         Gaps
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                     61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                       65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGLQTPQTFQGGTKVEIK 116
                                                                                       ;
0
                                                  83.7%; Score 498; DB 1; Length 117;
85.7%; Pred. No. 4.5e-44;
ive 3; Mismatches 13; Indels
                 12664 MW; 92CS7DC719E558B1 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                     239 AA
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QBNEKO;
                                                                                           Conservative
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117 1
117 AA;
                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                         96;
             SEQUENCE
                                                      Query Match
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NUCLEOTIDE SEQUENCE. MEDLINE=84191506; PubMed=6325927;

NCBI_TaxID=9606;

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Ig kappa chain V-II region GM607. Framework-1.

Complementarity-determining-2. Complementarity-determining-1.

Framework-2 Framework-3

1117 27 43 58 65 97 106 116

5 28 44 44 59 66 66 98 98 27

Complementarity-determining-3.

By similarity Framework-4.

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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Schwerz, Schnutz J., Myers R.M., Schnig A.S.N., Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Gener than 15,000 full-length human and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Expressed human immunoglobulin kappa genes and their hypermutation.";
Eur. J. Immunol. 23:3248-3262(1993).
EMBL; BC030814; AAH30814.1: -: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huber C., Klobeck H.G., Zachau H.G.; "Ongoing V kappa-J kappa recombination after formation of a productive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show somatic mutation.";
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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PIR; S236318; S23638.

PIR; S4012, S34091.

PIR; S40142; S40342.

PIR; S40357; S40357.

PIRSP, POR334; ITZZ.

SMR, Q8NEKO; 21-237.

INTERPRO; IPR007110; Ig-like.

INTERPRO; IPR003597; Ig_MHC.

INTERPRO; IPR003596; Ig_MHC.

INTERPRO; IPR003596; Ig_WHC.

INTERPRO; IPR003596; Ig_WHC.

INTERPRO; IPR00456; Ig_WHC.

INTERPROSITE; PS00406; Ig_WHC; UNKNOWN_1.
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ir. J. Immunol. 22:1561-1565(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Emmunoglobulin domain.
SEQUENCE 239 AA; 26
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Prostate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=1601042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=8436174
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RESULT 5

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TERY NO. Page D.L., Kimura S., Isobe T., Osserman E.F., Glenner G.G.;
Glenner G.G.;
Glentity of Bence Jones and amyloid fibril proteins in a patient with plasma cell dyscrasia and amyloidosis.";
D. Clin. Invest. 52:1276-1281(1973).
I. MISCELLANEOUS: The major amyloid protein appears to be identical with the Bence Jones protein isolated from the same patient.
I. MISCELLANEOUS: This protein was isolated from the surine of a patient with plasma cell dyscrasia and amyloidosis.
I. MISCELLANEOUS: The C region of this chain has the INV (1,2)
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                                                                                                                                                                                                                                                                                                                                                                 Putnam F.W., Whitley B.J. Jr., Paul C., Davidson J.N.;
"Amino acid sequence of a kappa Bence Jones protein from a case primary amyloidosis.";
Biochemistry 12:3763-3780(1973).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW). MEDLINE=73166638; PubMed=4700495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin V region.
                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Homo sapiens (Human).
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113 AA
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SMR; P01617; 1-113.

GO: 0005557; C:extracellular region; NAS GO; GO: 0005557; F:antigen binding; NAS.
GO; GO: 0006955; P:immune response; NAS.
InterPro: IPR007110; Ig-like.
InterPro: IPR003396; Ig-v.
SMART; SM0406; IGV; 1.
PROSTIF; PSSC935; IG_LIKE; 1.
Amyloid; Bence-Gones protein; Direct proteinmunoglobulin domain; Immunoglobulin V reg
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PRT;
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STANDARD;
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                                                                                                                                                                                                                                                                     NCBI TaxID=9606;
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1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novotny J., Margolies M.N.;
"Amino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma antibody.";
Blochemietry 22:1153-1158(1983).
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61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPPWTFGQGTKVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erlandsson A.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ884575; CAI56337.1; -; mRNA.
InterPro; IPR003599; Ig.
InterPro; IPR00310; Ig-like.
InterPro; IPR003596; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 AA; 12560 MW; E4D3BF3D63E88007 CRC64;
                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                               10-MAY-2005 (TrEMBLrel. 30, Last sequence upda
10-MAY-2005 (TrEMBLrel. 30, Last annotation up
Kappa light chain variable region (Fragment).
Name-19G1 anti-TS1 VL;
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21-JUL-1986 (Rel. 01, Last sequence update)
11-MAY-2005 (Rel. 47, Last annotation update)
19 kappa chain V-II region 26-10.
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                                                                                                                                                                                                                     Created)
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NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF07686; V-set; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                          QSF2IO MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huber C., Klobeck H.G., Zachau H.G.; "Ongoing V kappa-J kappa recombination after formation of a productive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr, Gaskin F., Fu S.M.;
"A rheumatoid factor from a normal individual encoded by VH2 and V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMZALQAPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MCLECTIDE SEQUENCE.
MEDLINE-98277139; PubMed-9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 114;
                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998).
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Eur. J. Immunol. 22:1561-1565(1992).
EMBL; ARO35034; AAD56270.1; -; mRNA.
PIR; B49002; B49002.
PIR; S23638; S23638.
PIR; S34094; S34094.
PIR; S34095; S34095.
HSSP; P01625; ILVE.
SMR; Q9UL80; 1-114.
                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eur. J. Immunol. 23:391-397(1993)
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InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=8436174;
Wagner S.D., Luzzatto L.;
                                                                                                                                                      QULBO HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene segments.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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A Altschul S.P., Zeeberg B. S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Robak S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,
A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                            HSSP, Q99M37; 1191.
Ensembl; ENSMUSG0000055315; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-v.
SWART; SM00406; IGv.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Monoclonal antibody.
                                                                                                                                                                                                                      Complementarity-determining-1.
                                                                                                                                                                                                                                            Complementarity-determining-2.
                                                                                                                                                                                                                                                        Framework-3.
Complementarity-determining-3.
Framework-4.
By similarity.
                                                                                                                                                                                                                                                                                                                                         Length 113,
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                                                                                                                                                                                                                                                                                                                  12273 MW; F9F39CE949A84C2A CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                       81.2%; Score 483; DB 1;
82.1%; Pred. No. 1.6e-42;
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            protein that binds digoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QETCDO_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                              92; Conservative
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54
61
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112
93
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                                                                                                  PIR; A01914; KVMS26.
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                                                                                                                                                                                                                                                                                                                113 AA;
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Matches 92; Conser
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SEQUENCE
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein R., Jaenichen R., Zachau H.G.; "Expressed human immunoglobulin kappa genes and their hypermutation."; Eur. J. Immunol. 23:3248-3262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=8416174; Magner S.D., Luzzatto L.; Magner S.D., Luzzatto L.; Magner S.D., Luzzatto L.; "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lauther-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F., Thiebe R., Zocher I., Zachau H.G.;
"The human immunoglobulin kappa locus. Characterization of the duplicated A regions." A regions. "Immunol. 22:1023-1029
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
Hyporhetical protein; Immunoglobulin domain.
SEQUENCE 239 AA; 26235 MW; FACEDC3A3B03871D CRC64;
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81.2%; Pred. No. 6.3e-42;
ive 12; Mismatches 9;
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InterPro; IPR003597; 19 c1.
InterPro; IPR003006; 19 MHC.
InterPro; IPR003596; 19 WHC.
Pfam; PF07654; C1-set; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S22658; S22658.
PIR; S34095; S34095.
PIR; S40324; S40324.
PIR; S40374; S40374.
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PIR; S42267; S42267.
PIR; S42268; S42268.
HSEP; P01884; 1172.
SWR; QBTCD0; 21-237.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                     PubMed=1598223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=1551402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUE
PubMed=8258341;
                                                                                                                                                                                        NUCLEOTIDE S
TISSUE=Lung;
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Query Match
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Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A popkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Butchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rabask S.A., McKwan P.J., McKernan R.J., Malek J.A., Gunstane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raber J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 SGVPDRFSGSGAGIDFTLKISRVEAEDVGVYYCMQVSHFPRTFGQGIRVEIK 132
                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.3%; Score 478; DB 2; Length 23 79.5%; Pred. No. 1.3e-41; tive 11; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC063599; AAH63599.1; -; mRNA. HSSP; P01837; IKCU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26245 MW; CD7313DDFFD358B3 CRC64;
                           vo-JUL-2004 (TrEMBLrel. 27, Created)
Hypothetical (TrEMBLrel. 27, Last sequence update)
Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Merann.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                          239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
                          PRT;
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InterPro; IPR00310; Ig-11ke.
InterPro; IPR00359; Ig c1.
InterPro; IPR003006; Ig c1.
InterPro; IPR003006; Ig WHC.
InterPro; IPR003596; Ig v.
Pfam; PF07654; C1-set; I.
SMART; SM00407; IG21; I.
SMART; SM00407; IG21; I.
                   QEP491 HUMAN PRELIMINARY;
QEP491;
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Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 protein.
239 AA; 2
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                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
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                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissum=Skin;
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                                                                                                                                                                                                    TISSUE=Skin;
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             HUMAN
RESULT 10
             Q6P491
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MEDLINE-22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;
X Strausberg R.L., Fearbaold B.A., Groube L.H., Derge J.G.,
A Strausberg R.L., Fearbaold B.A., Groube L.H., Derge J.G.,
A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Lownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Brownstein M.J., Workernan K.J., Malek J.A., Gunaratne P.H.,
R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
R Aniting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
R Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
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                                                                                                                                                          Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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5; Mismatches 15
240 AA
PRT;
                                                                                                         Created)
                                                                                             05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.48;
QEPIHE_HUMAN PRELIMINARY;
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                                                                                                                                                                                                                                                        IGKV1-5 protein.
Name=IGKV1-5;
Homo sapiens (Human).
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KV2A_HUMAN

RESULT 11

RESULT 12

us-10-735-916a-61.rup

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Best Local Similarity
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00406; IGV; 1.—PROSITE; PS50835; IG_LIKE; 1.
Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   $\tilde{O53VPB}$ MOUSB PRELIMINARY; PRT; 112 AA.
$\tilde{O53VPB}$
$\tilde{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 DIVMTQTPLSLPVTPGEPASISCRSSQSLLDSGDGNTYLNWYLQKAGQSPQLLIYTLSYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular basis of antibody formation.";
Naturwissenschaften 56:195-205(1969).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHS-NGNTYLQWYLQKPGQSPQLLIYKVSNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 LYGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 ASGVPDRFSGSGSGTDFTLKISRVQAEDVGVYYCMQRLEIPYTFGQGTKLEIR 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12676 MW; 59E9F90A379569EC CRC64;
                                                                                                                                                                                                                                                                                                                                                              Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967)
                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUX-2005 (Rel. 47, Last annotation update)
19 kappa chain V-II region Cum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSP, P01751; INQB.
SMR; P01614; 2-115.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
  115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE REVISION TO 50; 52; 96 AND 97.
MEDLINE=70063440; Pubmed=4188189;
                                                                                                                                                                                                                                                                        MEDLINE=68242259; PubMed=5586923;
Hilschmann N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 79.6
nes 90; Conservative
  STANDARD;
                                                                                                                           Homo sapiens (Human).
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115 AA;
                                                                                                                                                                                                                                                    PROTEIN SEQUENCE.
                                                                                                                                                                                                            NCBI_TaxID=9606;
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  KV2A HUMAN
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SEQUENCE
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RA Kipp B., Schlaak M., Becker W.M.;

Kipp B., Schlaak M., Becker W.M.;

"Cloning and expression of a recombinant mouse Fab-fragment
recognizing and defined linear epitope of Chironomus thummi major
recognizing a defined linear epitope of Chironomus thummi major
recognizing a defined linear epitope of Chironomus thummi major
RT Int. Arch. Allergy Immunol. 110:348-353(1996).

REMBI. 237499; CAA885724.1; -; mRNA.

REMBI. 237499; CAA885724.1; -; mRNA.

REMBI. 237499; CAA885724.1; -; mRNA.

REMPI. 187003109; IG.

RICEPPO: IPR003106; IG.

RICEPPO: IPR003106; IG.

RICEPPO: IPR003596; IG.

RICEPPO: IPR003596; IG.

REMBI. SWART; SW00409; IG. 2.

SWART; SW00400; IG. 2.

SWART; SW00406; IGV. 1.

REMBIRE PSS0835; IG.LIKE; 2.

REMSITE; PSS0835; IG.LIKE; 2.

REMSITE; PSS0835; IG.LIKE; 2.

REMSITE; PSS0835; IG.LIKE; 2.
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                                                    NUCLEOTIDE SEQUENCE.
MEDLIFFE-86136012; PubMed=3937730;
MEDLIFFE-86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
The idiotypic network and the internal image: possible regulation of a germ-line network by pauchgene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
EMBO J. 4:3681-3688 (1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                            Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03386; CAA27113.1; -; mRNA.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                               112 112
112 AA; 12266 MW; C844B7881A89C18A CRC64;
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Last annotation update)
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Pred. No. 2.1e-40;
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25-OCT-2004 (TrEMBLrel. 28, Last seque
25-OCT-2004 (TrEMBLrel. 28, Last anno
Kappa light chain C region (Fragment)
Mus musculus (Mouse).
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STRAIN=Balb/c; TISSUE=Spleen;
MEDLINE=96319505; PubMed=8768802;
                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE OF 108-109.
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79.5%;
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Q65ZC0;
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219 AA;
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NCBI_TaxID=10090,
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Riesen W.F., Jaton J.-C.;
"Variable region sequence of the light chain from a Waldenstroms IgM with specificity for phosphorylcholine.";
Biochemistry 15:3829-3833(1976).
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                                                                                                                                                           -i- MISCELLANEOUS: This chain was isolated from a Waldenstrom's macroglobulin that binds phosphorylcholine.
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Complementarity-determining-3.
Framework-4.
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12; Indels
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PROSITE; PS50835; IG LIKE; 1.
Direct protein aequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Homo sapiens (Human).
  11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMR; P01615; 1-109.

SMR; P01615; 1-109.

GO; GO:0005576; C:extracellular region; NAS.

GO; GO:0003823; F:antigen binding; NAS.

GO; GO:0006955; P:immune response; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR00356; Ig-v.
                                                                                                                                                                                                                                                                                                                                                            113 AA.
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MEDLINE=76253627; PubMed=821524;
  89; Conservative
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NCBI_TaxID=9606;
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61 SGVPDRFSDSGSGTDFTLKITRVQAEDVGVYYCMQATZSPYTFGQGTKLZIK 112
                                                                  Search completed: January 10, 2006, 20:53:25
Job time: 75.5025 secs
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January 10, 2006, 20:07:41; Search time 77.3134 Seconds (without alignments) 636.505 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                        2443163 segs, 439378781 residues
                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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geneseqp20008:* geneseqp20018:* geneseqp20028:* geneseqp2003a8:* geneseqp2003b8:* geneseqp1980s:* geneseqp1990s:* geneseqp2004s:* geneseqp2005s:* ۱.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Adj76895 Anti-IGF-Adz67065 Human ant Adj76899 Anti-IGF-Adz67069 Human ant Adj76899 Anti-IGF-Adz67069 Human ant Adj84960 Variable Adz67071 Human ant Adj84960 Variable Human ant Anti-IGF-Human ant Anti-IGF-Human ant Variable Mouse mon FGF-8 rel Mouse mon Mouse mon Humanised Description AAE15713 AAE15712 ADP84948 ADP84951 ADE36530 ADP84949 AAY42969 ADP84944 ADP84947 ADJ76899 ADZ67069 ADJ76901 AAE15711 ABP72125 ADE36495 ADJ76897 ADZ67067 ADZ67071 ADP84950 ADP84946 BB Query Match Length 1000.0 10000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1 Result Š.

	Ade36520 Anti-FGF-	Adv67310 Amino aci	Aar32239 Humanised	Aaw27145 Mature li	Aay87571 Humanised		Adp84945 Variable			Adp84943 Variable	Adj80420 Hybrid hu	Adh61998 Human ant	Abr40272 Amino aci	_	Adz52552 Anti-CCR4	Abr40268 Amino aci	Ade27687 Humanised	Ade36519 Anti-FGF-	Ade36527 Anti-FGF-	Adj80422 Murine an
6 ABP72129	7 ADE36520	9 ADV67310	2	2 AAW27145	3 AAY87571	2 7 ADE36522	8 ADP84945	8 ADP84952	2 7 ADE36518	8 ADP84943	2 7 ADJ80420	2 7 ADH61998	2 6 ABR40272	2 7 ADE27694	6	2 6 ABR40268	2 7 ADE27687	2 7 ADE36519	7	7 4
93.6	93.6	93.6	93.4	93.4	93.4	93.4	93.4	93.3	92.9	92.8	92.4	92.4	91.9	91.9	91.9	91.8	91.8	91.8	546 91.8 112	. 0
25	52	27	58	53	30	31	32	1 6	34	35	36	37	38	6 6	40	41	4.2	4.3	4 4	45

ALIGNMENTS

RESULT

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Geneseq 21:*

Database :

insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; cytostatic; antipsoriatic; antibody; ADJ76895 standard; protein; 112 AA Anti-IGF-1R related protein #12. (first entry) WO2003059951-A2 Homo sapiens. 24-JUL-2003. 06-MAY-2004 ADJ76895; ADJ76895

20-JAN-2003; 2003WO-FR000178

18-JAN-2002; 2002FR-00000653. 18-JAN-2002; 2002FR-00000654. 07-MAY-2002; 2002FR-00005753.

(FABR) FABRE MEDICAMENT SA PIERRE.

Leger 0; Corvaia N, Goetsch L,

WPI; 2003-569653/53.

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

Disclosure; SEQ ID NO 61; 164pp; French

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of

N-PSDB; ADZ67066.

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          transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF. IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                            Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; light chain variable region.
                                                                                                                                                                               1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                                                                  1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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                                                                                                                                                                                                                                                                                                                                                                                                     Human antibody 7C10 1 light chain variable region SEQ ID NO:61.
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                                                                                                                             Length 112;
these receptors with their ligands. Especially they inhibit
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2002FR-00005753.
2003WO-FR000178.
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/note= "CDR3"
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                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                       Matches 112; Conservative
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/note= "
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94. .10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-321968/33.
                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DUFLOS A. HABUW J.
                                                                                                     Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2005084906-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ното варіепв.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JAN-2002;
07-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                    ADZ67065;
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(HAEU/)
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activation of the transduction pathway of the signal mediated by the interaction of 1GF1 or 1GF2 with 1GF1R and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended coraracter, preferably 1GF-dependent, especially 1GF1 and/or 1GF2.

Conhibit the transformation of normal cells into cells with tumoral capandent and/or EGF-dependent, especially 1GF1 and/or 1GF2.

Consector, preferably 1GF-dependent and/or HERZ/neu-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or 1GF2-dependent and/or 1G
                                                                                                                                                                                                                                                                                     I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADS67006 and ADS67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of IGF-
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                                              Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGI and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                            relates to a novel isolated anti-insulin-like growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 595; DB 9;
100.0%; Pred. No. 2.4e-43;
ive 0; Mismatches 0;
                                                                                                                                                                                                        Example 12; SEQ ID NO 61; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ76897 standard; protein; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-IGF-1R related protein #13.
                                                                                                                                                cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 112; Conservative
                                                                                                                                                   for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
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insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway;

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light chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrise; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 DVVWTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 79
   ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                         New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human antibody 7C10 1 light chain variable region SEQ ID NO:63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein sequence used to generate the Ab of the invention
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100.0%; Pred. No. 2.9e-43;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 63; 164pp; French.
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                                                                                                                                                                                           18-JAN-2002; 2002FR-0000653.
18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                           20-JAN-2003; 2003WO-FR000178
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Best Local Similarity 100.
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                          WPI; 2003-569653/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 131 AA;
                                                                                     WO2003059951-A2
                                                     Homo sapiens.
                                                                                                                        24-JUL-2003
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human 1GF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with assistance of the remarkation of the transduction pathway of the signal mediated by the interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin conceptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral consecutor, preferably IGF-dependent and/or HERZ/neu-dependent cells, in is useful in the proparation of two I thumor cells, preferably IGF-dependent and/or EGF-dependent and/or EGF-dep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (1) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriasis. (1) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leger O, Duflos A, Haeuw J, Beck A;
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                                                                                                                      .. .19
'note= "leader peptide"
                                                                          location/Qualifiers
                                                                                                                                                                               .62
.-- "CDR1"
                                                                                                                                                                                                                                                                            74. .80
/note= "CDR2"
113. .121
/note= "CDR3"
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07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
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2002FR-00000654
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N-PSDB; ADZ67066.
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
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Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-APR-2005.
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                                                                                   Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GOET/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LEGE/)
                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                         Region
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osteosarcoma, and

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cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                          79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                        DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                             DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                               YGVPDRFSGSGSGTDFTLKISRVBABDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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0
                                                                                                                                                                                     Length 131;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                    Score 595; DB 9;
Pred. No. 2.9e-43;
                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; antipsoriatic; antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ76899 standard; protein; 112
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100.0%;
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07-MAY-2002; 2002FR-00005753.
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                                                                                                                                                                                                                       Matches 112; Conservative
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                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                  Sequence 131 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of
          also for treating psoriagis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
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                                                                                                                                                                              DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                 Gaps
                                                                                                                                                                                                                       YGVPDRFSGSGSGTDFTLKISRVBAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                          YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                    Human antibody 7C10 2 light chain variable region SEQ ID NO:65
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                                                                                                  99.8%; Score 594; DB 7; Length 112; 99.1%; Pred. No. 3e-43;
                                                                                                                                 0; Indels
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prostate, lung, breast, endometrium and colon, also
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                                                                                                                                 1; Mismatches
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                                                                                                                                                                                                                                                                                                                             ADZ67069 standard; protein; 112
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07-MAX-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
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CORVAIA N.
LEGER O.
                                                                                                                  Similarity
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                                                                      Sequence 112 AA;
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                                                                                                    Query Match
Best Local
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(BECK/)
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comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An autibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of a milness connected with an overexpression and/or an abnormal contivation of the IGF-IR and/or connected with a moverextron of IGF or IGF-IR and/or connected with a cityation of the IGF-IR and/or EGFR, and/or of EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2-dependent and/or IREZ/neu-dependent cells. (I) is useful for preparation of a medicament intended for IGF1 and/or IGF-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to resumble of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to resume the invented in vierto diagnosis of illnesses induced by an undersored in the IGF-IR and/or IGF-IR IGF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         starting from a biological sample in which the abnormal presence, of IGP-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        overexpression or an underexpression of the IGF-IR and/or EGFR receptor
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99.8%; Score 594; DB 9;
Best Local Similarity 99.1%; Pred. No. 3e-43;
Matches 111; Conservative 1; Mismatches
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or creat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of numor cells to tumor cells, inhibit growth and/or prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; light chain variable region.
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                                                                                                                                                                                                                                                                                       New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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Pred. No. 3.5e-43;
1; Mismatches 0; Indels
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/note= "leader peptide"
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/note= "CDR2"
113. .121
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/note= "CDR1"
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                               2002FR-00005753
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18-JAN-2002; 2002FR-00000654
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                                                                                                                                                                                                                           WPI; 2003-569653/53.
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Best Local Similarity
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                               07-MAY-2002;
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receptor (IGF-IR) antibody (I) or its functional fragment, being capable of capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal cyperactivation of the IGF-IR and/or Connected with a hyperactivation of the IGF-IR and/or Connected with a hyperactivation of the transduction pathway of the signal mediated by the interaction of IGF or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells with tumoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             character, preferably IGF-dependent, especially IGF1 and/or IGF2.

dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful for preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent, especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer, encourage of the cancer, encourage of the cancer, encourage of the prevention or for the preparation of a medicament intended for the prevention or for the preparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an electric cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-and appecifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duflos A, Haeuw J, Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 12; SEQ ID NO 67; 125pp; English.
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/note= "CDR3"
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2002FR-00005753.
2003WO-FR000178.
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CORVAIA N.
LEGER O.
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(HAEU/)
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Score 594; DB 9; Pred. No. 3.5e-43; 99.8**%**; 99.1**%**; Query Match Best Local Similarity Sequence 131 AA;

Length 131;

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This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition molecules are used to make constructs containing the framework regions that be specified eadvor flank the specified sequences, especially where the framework regions are from the immunoglobulin [Ig] superfamily, protease inhibitors, lectins, helix-bundle proteins and/or lipocalins. Wost especially the framework regions are from antibodies, particularly the variable heavy chain (VH) and the variable light chain (VL) of human and/or murine origin. The constructs may also include a His or myc tag, a lysine-rich region and/or a multimerisation domain, most particularly it is a single-chain antibody fragment, with peptide or protein, and/or an Ig of types G, M, A, B or D and/or their subclasses. It may be human, thumine or chimerised, murine or chimeric, e.g. IgM without the J chain. The additional sequences/structures in the constructs are Ig domains of various species, interacting or stabilising domains, signal sequences, fluctuated in the constructs are Ig domains of various species, cytolytic agents, enzymes, immuno-modulators or effectors, MHC molecules, antigens, chelators for radioactive labels, liposomes, transmembrane domains, viruses and/or cells, specifically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recognition molecules, e.g. antibodies (and nucleic acids) that bind specifically to Core-1 antigens, useful for diagnosis, treatment and prevention of tumors and metastases.
                                       20 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 79
                                                                                                                                                                                                                                                                                                                                                                                                 antibody; Core-1 antigen; framework region; immunoglobulin superfamily; protease inhibitor; lectin; helix-bundle protein; lipocalin; variable heavy chain; Wiy variable light chain; Wi, vaccine; diagnosis; alleviation; treatment; tumour; breast; colon; stomach; pancreas; large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                   YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                           80 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 131
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                                                                                                                                                                                                                                   ADP84950 standard; protein; 114
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                                                                                                                                                                                                                                                                                                                      09-SEP-2004 (first entry)
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Christensen PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus.
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Chimeric.
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                   acid encoding them, and related vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment, monitoring and/or secondary treatment of tumours (specifically of breast, colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or liver) and/or metastases (particularly to liver), specifically where these are positive for the Cl antigen. The products of the invention provide simple, reliable and efficient detection of tumours. They are specific for carcinoma and show almost no binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; humanised form; monoclonal antibody alpha 340; gene therapy; epidermal growth factor receptor; BGF; cancer; colorectal; lung; breast; gastric; ovarian; immune response; cytostatic; cell growth; apoptosis; inhibitor; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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macrophages. The antibodies, also constructs containing them, nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCFQGSHVPYTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 569; DB 8; Length 114;
Pred. No. 4.2e-41;
3; Mismatches 2; Indels
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24-AUG-2000; 2000GB-00020794.
                                                                                                                                                                                                                                                                                                                                                                                                             95.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                 Sequence 114 AA;
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                                                                                                                                                                                                                                                                                      healthy tissue.
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Synthetic.
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Best Local S
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mouse monoclour antibody which binds to epidermal growth factor (EGF)
creeptor and inhibite binding of EGF), obtainable from the cell line
creeptor and inhibite binding of EGF), obtainable from the cell line
deposited with the ECACC under accession number 9702148. The humanised
CC form of the antibody 340 is useful in gene therapy, medicine and in the
cmanufacture of a medicament for treatment or prophylaxis of cancer. The
invention is useful for treating colorectal, lung, breast, gastric or
covariant cancers or also for preventing the recurrence of cancer after
initial treatment or surgery. The invention is also useful for enhancing
a protective immune response against cancer by optimised immunisation
cs schedules. The humanised form of the antibody 340 has reduced
immunogenicity but shows similar binding to cells expressing EGF
creeptor, as the original murine antibody and has increased ability to
inhibit the growth and apoptosis inhibitor. The present sequence is
mouse monoclonal antibody alpha 340 deimmunised light chain variable (VK)
region variant, 340VKd
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                                                                                                      New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; humanised form; monoclonal antibody alpha 340; gene therapy; epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast; gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;
                                                                                                                                                                                                                          present invention relates to a humanised form of the antibody 340 (a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVIMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse monoclonal antibody alpha 340 Vk region variant, 340VKc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.5%; Score 56%; DB 5; Length 112; 94.6%; Pred. No. 5e-41; ive 3; Mismatches 3; Indel8
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                                      Durrant LG;
(SCAN-) SCANCELL LID.
                                                                      WPI; 2002-062384/08.
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antibody; Core-1 antigen; framework region; immunoglobulin superfamily; protease inhibitor; lectin; helix-bundle protein; lipocalin; variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis; alleviation; treatment; tumour; breast; colon; stomach; pancreas; large/small intestine; ovary; cervix; lung; prostate; kidney; liver;

Variable light chain VL fragment Karoll SEQ ID NO 90.

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The present invention relates to a humanised form of the antibody 340 (a mouse monoclonal antibody which binds to epidermal growth factor (EGF) receptor and inhibits binding of EGF), obtainable from the cell line deposited with the ECACC under accession number 97021428. The humanised form of the antibody 340 is useful in gene therapy, medicine and in the manufacture of a medicament for treatment or prophylaxis of cancer. The invention is useful for treating colorectal, lung, breast, gastric or ovarian cancers or also for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing a protective immune response against cancer by optimised immunisation acchedules. The humanised form of the antibody 340 has reduced immunogenicity but shows similar binding to cells expressing EGF receptor, as the original murine antibody and has increased ability to inhibit the growth of EGF receptor expressing cells. The invention is used as cell growth and apoptosis inhibitor. The present sequence is mouse monoclonal antibody alpha 340 deimmunised light chain variable (VK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer.
                                      "Wild type Lys substituted with Gln"
                                                                                                                                                                                                /note= "Wild type Asn substituted with Lys"
"Wild type Gln substituted with Pro"
                                                                                                                                                           note= "Wild type Leu substituted with
                                                                                                                    note= "Wild type Ile substituted with
                                                                             "Wild type Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Fig 7; 53pp; English.
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                                                                                                                                                                                                                                                                                                                                                          19-MAY-2000; 2000GB-00011981
24-AUG-2000; 2000GB-00020794
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ellis JRM, Durrant LG;
                                        note=
                                                                                 note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region variant, 340VKc
                                                                                                                                                                                                                                                                                                                                                                                                                     (SCAN-) SCANCELL LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-062384/08.
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                                                           Misc-difference
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                  Misc-difference
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Stahn

Danielczyk A, Karsten U, Ravn P,

Christensen PA;

Goletz S,

(NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG

01-DEC-2003; 2003WO-DE003994. 29-NOV-2002; 2002DE-01056900.

WO2004050707-A2

17-JUN-2004

Mus musculus gapiens

Chimeric.

metastasis.

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                                                                                1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                       1 DVLMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRF
                                         Gaps
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                                                                                                                                                                                   SGVPDRFSGSGSGTDFTLKISRVEAEDTGVYYCFQGSHVPWTFGGGTKVEIK 112
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95.0%; Score 565; DB 5; Length 112; 94.6%; Pred. No. 9.1e-41; ive 2; Mismatches 4; Indels
                                         Conservative
                  Similarity
                                     106;
Query Match
                      Local
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This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition molecules are used too make constructs containing the framework regions that separate, include and/or flank the specified sequences, especially where the framework regions are from the immunoglobulin [1g] superfamily, both especially the framework regions are from antibodies, particularly the variable heavy chain (VH) and the variable light chain (VL) of human and/or murine origin. The constructs may also include a His or myc tag, a shigle-chain antibody fragment, multibody, Pab fragment, fusion protein of an antibody fragment, multibody, Pab fragment, fusion protein of an antibody fragment with peptide or protein, and/or an Ig of types G, M, A, E or D and/or their subclasses. It may be human, humanised, murine or chimeric, e.g. IgM without the J chain. The additional sequences/structures in the constructs are Ig domains of various species, interacting or stabilising domains, signal sequences, to specificities, cytolytic agents, enzymes, immuno-modulators or cherry specificaties, cytolytic agents, enzymes, immuno-modulators or cherry specificaties, the antibodies with catalytic activity or other specificaties of an antibodies, also constructs containing them, nucleic acide an area as and an area and an area transments on transment to a severely or chain the constructs containing them, and related vectors and host cells, are useful for an area and an area to a severely or an area of the antibodies with cataly in transments on transments on transments on transments on transments and order on transments on transments on transments and order on transments on transments and order on transments on transments on transments and order on transments on transments on transments or transments or an area of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recognition molecules, e.g. antibodies (and nucleic acids) that bind specifically to Core-1 antigens, useful for diagnosis, treatment and prevention of tumors and metastases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; SEQ ID NO 90; 136pp; German.
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1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60

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Gaps ; 0

Length 114;

Score 565; DB 8; Length 11: Pred. No. 9.2e-41; 4; Mismatches 2; Indels

95.0%; 94.6%;

Matches 106, Conservative

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Query Match Best Local Similarity

ADP84948 standard; protein; 114 AA

RESULT 12

(first entry)

09-SEP-2004

ADP84948;

ADP84948
ID ADP8
XX
AC ADP8
XX
DT 09-S

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New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer.
                                                                                                                                                                                                                                                      Mouse; humanised form; monoclonal antibody alpha 340; gene therapy; epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast; gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a humanised form of the antibody 340 mouse monoclonal antibody which binds to epidermal growth factor (EGF)
SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPYTFGQGTKVEIK 112
                                            61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                             Mouse monoclonal antibody alpha 340 VK region variant, 340VKb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Wild type Asp substituted with Glu"
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                                                                                                                                                                                                                                                                                       gastric; ovarian; immune response;
inhibitor; mutant; mutein; variant.
                                                                                                                                             AAE15711 standard; protein; 112 AA
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24-AUG-2000; 2000GB-00020794
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Synthetic.
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                                                                                                               RESULT
AAE1571
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receptor and inhibits binding of EGF), obtainable from the cell line deposited with the ECACC under accession number 9701428. The humanised for antibody 340 is useful in gene therapy, medicine and in the manufacture of a medicament for treatment or prophylaxis of cancer. The invention is useful for treating colorectal, lung, breast, gastric or ovarian cancers or allos for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing a protective immune response against cancer by optimised immunisation cachetive immune response against cancer by optimised immunisation is chedules. The humanised form of the antibody 340 has reduced immunisation is ceptor, as the original murine antibody and has increased ability to immunish the growth of EGF receptor expressing cells. The invention is used as cell growth and apoptosis inhibitor. The present sequence is mouse monoclonal antibody alpha 340 deimmunised light chain variable (VK)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel humanised antibodies and antibody fragments which react with fibroblast growth factor 8 (FGF8) and inhibit its biological functions. The polypeptides of the invention have cytostatic activity. The antibody is useful for the treatment of cancer, including prostate, breast, ovarian and testicular cancer. The present sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised; antibody; fibroblast growth factor 8; FGF8; cytostatic; cancer; prostate; breast; ovarian; testicular.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGVPDRFSGSGSGTDFTLKISRVEAEDTGVYYCPQGSHVPWTFGGGTKVEIK 112
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Pred. No. 1.3e-40;
3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP72125 standard; protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGF-8 related protein SEQ ID 17.
                                                                                                                                                                                                                                                                                                                                              94.6%;
93.8%;
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Matches 105; Conservative
                                                                                                                                                                                                                                                                      region variant, 340VKb
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                                                                           1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                              The invention comprises a method for treating and preventing arthritis, the method involves the use of anti-FGF-8 (sic fibroblast growth factor) antibody. The antibody and method of the invention is useful for: the detection, treatment and prevention of arthritis; as a cartilage protection agent; as a joint destruction inhibitor; and as a synoviral proliferation inhibitor. The present amino acid sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment and prevention of arthritis comprising the use of anti-FGF-8 (sic fibroblast growth factor) antibody.
                                                                                                                                                                                                                                                                                                                                             Anti-FGF-8 (sic fibroblast growth factor) antibody-related protein #2.
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                                              Gaps
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                Length 112;
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                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                      arthritis; anti-FGF-8; sic fibroblast growth factor; cartilage protection agent; joint destruction inhibitor; synoviral proliferation inhibitor.
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Best Local Similarity 93.8%; Pred. No. 1.3e-40;
Matches 105; Conservative 5; Mismatches 2.
              Score 563; DB 6;
Pred. No. 1.3e-40;
   94.6%; Scor.
93.8%; Pred. No. 1....
5; Mismatches
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                                                                                                                                                                                                                                                 ADE36495 standard; protein; 112 AA
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                              Best Local Similarity 93.8
Matches 105; Conservative
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Search completed: January 10, 2006, 20:44:14

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YGVPDRPSGSGSGTDFTLXISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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Best Local Similarity 100.0
Matches 112; Conservative
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                                                                       January 10, 2006, 20:55:23; Search time 5.71144 Seconds (without alignments) 166.558 Million cell updates/sec
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                                                                                                                                                   1 DVLMTQIPLSLPVSLGDQAS......CFQGSHVPWTFGGGTKLEIK 112
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1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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US-11-012-353-56
US-11-089-266-66
US-11-089-266-15
US-11-012-353-57
US-10-012-353-57
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US-10-012-353-67
US-10-512-184-67
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US-10-932-334-8
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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Sequence Seq
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100.0%; Pred. No. 1.1e-39;
tive 0; Mismatches 0;
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US-11-125-837-23
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                                                                             GEMERAL INFORMATION:

APPLICANT: GOETSCH, LILIANE
APPLICANT: GOETSCH, LILIANE
APPLICANT: GOETSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HABUW, JEAN-FRANCOIS
APPLICANT: HABUW, JEAN-FRANCOIS
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVERER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR PLILING DATE: 2003-07-11
PRIOR FILING DATE: 2002-01-08
PRIOR PLILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PACENTIN VERSER: FR 0200653
SPRIOR PLILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PACENTIN VERS: 3.3
SEQ ID NO 49
LENGTH: 122
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Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTSCH. LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HEERW, OLIVIER
APPLICANT: BECK, ALAIN
APPLICANT: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
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CURRENT FILING DATE: 2004-12-16
PRIOR PRILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR FILING DATE: 2003-01-20
PRIOR PLING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: PR 0205753
                     Sequence 49, Application US/11012353
Publication No. US20050249730A1
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Best Local Similarity 100.0
Matches 112; Conservative
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ORGANISM: Mus musculus
                                                                  GENERAL INFORMATION:
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US-11-012-353-56
-11-012-353-49
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20 DVLATQTPLSLPVSLGDQASISCRSSQSIVNSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DVLATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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Sequence 66, Application US/11089266

Publication No. US20050287148A1

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya

APPLICANT: Foon, Kenneth A.

TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE

TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YGVPDRFSGSGSGTDFTLKISSVBAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCPQGSHVPWTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.6%; Score 564; DB 7; Length 112; Best Local Similarity 95.5%; Pred. No. 1.1e-37; Matches 107; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lin, Rong-Hwa
APPLICANT: Chang, Chung Nan
APPLICANT: Chang, Chung Nan
APPLICANT: Chang, Chung Nan
APPLICANT: Chang, Chiu-Chen
TITLE OF INVENTION: ANTIBODIES
FILE REFRENCE: 13062-011001
CURRENT APPLICATION NUMBER: US/11/125,837
CURRENT FILING DATE: 2005-05-10
PRIOR PLING DATE: 2004-05-10
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PASSEQ for Windows Version 4.0
SERGTH: 131
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 23, Application US/11125837; Publication No. US20050266003A1; GENERAL INFORMATION:
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Best Local Similarity 94.6
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-23
                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus US-11-012-353-56
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQXPGQSPKLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 93.4%; Score 551; DB 7; Length 263; Best Local Similarity 93.8%; Pred. No. 2.1e-36; Matches 105; Conservative 1; Mismatches 6; Indels
                                            CITY:
CITY:
CITY:
COUNTRY: USA

ZIP: 94304-101
ZIP: 94304-101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATR:
APPLICATION NUMBER: US/11/089,266
FILING DATE: 23-Mar-2005
FILING DATE: 23-Mar-2005
FILING DATE: 23-Mar-2005
FILING DATE: 1999-04-15
APPLICATION NUMBER: US/01/153,401
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
ATTORNEY/AGENT INFORMATION:
NAME: Catherine M. POlizzi
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
TELEOMOUNICATION INFORMATION:
                      E: MORRISON & FOERSTER
755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 706141
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein
US-11-089-266-66
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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1 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKKGQSPKLLIYFVSNRF 60
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/089,266
FILING DATE: 23-Mar-2005
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/153,401
FILING DATE: 27-Aug-2002
APPLICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1999-01-16
APPLICATION NUMBER: US 08/391,196
FILING DATE: 1996-01-16
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
APPLICATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
TELECOMMUNICATION INFORMATION:
TELEFORME (415) 813-5600
TELEFRAK: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 93.8 Matches 105; Conservative
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MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                       1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                 61 YGVPDRFSGSGSGTDFTLKISSVBAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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                                                                                                                                                                                                                                  Length 112;
                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 69, Application US/10932334
Publication No. US20050249728A1
GENERAL INFORMATION:
APPLICANT: ImmunoGen, Inc.
TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILE REFERENCE: A6689
CURRENT APPLICATION NUMBER: US/10/932,334
CURRENT PILING DATE: 2004-09-02
PRIOR PILIOR DATE: 2003-12-08
PRIOR PILIOR DATE: 2003-12-08
PRIOR PILIOR DATE: 2003-12-08
PRIOR PILIOR DATE: 2003-16-14
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 69
LENGTH: 113
                                                                                                                                                                                                                             Score 547; DB 7;
Pred. No. 2.2e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC FEATURE
LOCATION: (28)...(28)
OTHER INFORMATION: "X" may be any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC FEATURE
1 LOCATION: (101)...(101)
2 OTHER INFORMATION: "X" may be any amino acid
US-10-932-334-69
                                                                                                                                                                                                                             Query Match
92.7%; Score 547; DE
Best Local Similarity 92.0%; Pred. No. 2.2e
Matches 103; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                  PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 57
LENGTH: 112
PRIOR APPLICATION NUMBER: FR
                                                                                                                                      ; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-57
                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-932-334-69
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US-11-089-266-2
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Sequence 2, Application US/11089266 Publication No. US20050287148A1 GENERAL INFORMATION:

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1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 DVFWTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIXFVSNRF 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 55, Application US/11012353
Sequence 55, Application US/11012353
GENERAL INFORMATION:
APPLICANT: GOSTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
APPLICANT: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
APPLICANT: FOON, Kenneth A.
APPLICANT: FOON, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDENCES 66
CORRESPONDENCES: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YGVPDRFSGSGGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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Pred. No. 2.7e-36;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                          COMPUTER: 0.08

CONDITION: 0.08

CIP: 94304-1018

COMPUTER READABLE FORM: MEDIUM TYPE: Floopy disk

COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/11/089,266

FILING DATE: 23-Mar-2005

CLASSIFICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/10/153,401

FILING DATE: 129-40-105
APPLICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1995-01-16
ATTORNEY/AGENT INFORMATION:
NAME: Catherine M. Polizzi
REGISTRATION NUMBER: 304142000202
TELERBHONE: (415) 819-560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 92.9%;
Matches 104; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (415) 813-5600
(415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 149 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-11-089-266-2
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US-11-012-353-55
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US-10-512-184-30
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                                                                                                                                                                                                                                                                                                      SEQ ID NO 30
LENGTH: 251
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                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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Publication No. US20050249728A1

GENERAL INFORMATION:

TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY

FILE REFERENCE: A8689

CURRENT APPLICATION NUMBER: US/10/932,334

CURRENT PILING DATE: 2004-09-02

PRIOR FILING DATE: 2003-12-08

PRIOR FILING DATE: 2003-12-08

PRIOR FILING DATE: 2003-12-08

PRIOR FILING DATE: 2003-06-14

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 61

LENGTH: 113
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               CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 10/735,916
PRIOR PILING DATE: 2003-12-16
PRIOR PLILNG DATE: 2003-12-16
PRIOR PLILNG DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR APPLICATION NUMBER: FR 020573
PRIOR PLILNG DATE: 2003-01-20
PRIOR PLILNG DATE: 2002-01-18
PRIOR PLILNG DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 020653
PRIOR PLILNG DATE: 2002-01-18
PRIOR PLILNG DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
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Matches 103; Conservative
FILE REFERENCE: 017753-198
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US-11-012-353-55
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US-10-932-334-61
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LENGTH: 112
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Sequence 67, Application US/10512184

Publication No. US20050244901A1

GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REPERENCE: 3581.010501
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT PILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72

SOFTWARE: Patentin Ver. 2.1
Sequence 30, Application US/10512184
Sequence 30, Application US/10512184
Publication No. US20050244901A1
REMERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REPERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: scFv VD2 with OTHER INFORMATION: specificity against Verticillium dahliae; OTHER INFORMATION: originates from Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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11267 SGVPARFSGSGSGTDFTLKISRVBAEDLGVYYCFQGSHVPYTFGGGTKLEIK 318
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT PPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: PRECENTIFICIAL Sequence
CNGANISM: Artificial Sequence
                                                                                                     APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistence against fungi
FILE REFERENCE: 3581.01US01
CURRENT PRILIG DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SEG ID NOS: 72
SEQ ID NO 66
LENGTH: 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: precursor OTHER INFORMATION: fusion protein comprising chitinase - linker OTHER INFORMATION: SCFV VD2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.0%; Score 543; DB 6; Length 569; 92.9%; Pred. No. 1.6e-35; ive 2; Mismatches 6; Indels
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92.0%; Score 543; DB 6;
Best Local Similarity 92.9%; Pred. No. 1.8e-35;
Matches 104; Conservative 2; Mismatches 6
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                        Sequence 66, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 104; Conservative
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US-10-512-184-66
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Search completed: January 10, 2006, 21:36:22 Job time : 5.71144 secs

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27, Appl
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590
1 DVLMTQIPLSLPVSLGDQAS......CFQGSHVPWTFGGGTKLEIK 112
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/cgn2_6/ptodata1/iaa/5_COMB.pep:*
/cgn2_6/ptodata1/iaa/6_COMB.pep:*
/cgn2_6/ptodata1/iaa/H_COMB.pep:*
/cgn2_6/ptodata1/iaa/PGTUS_COMB.pep:*
/cgn2_6/ptodata1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata1/iaa/RE_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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S-08-591-15
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S-08-591-23-53-2
S-08-497-312-18
S-08-311-394-67
S-08-311-394-67
S-08-311-394-67
S-08-311-394-66
S-09-756-2194-190
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US-08-859-649-29
US-08-207-861-19
US-08-207-861-29
US-08-859-648-19
US-09-192-545-4
US-09-131-398A-48
US-08-331-398A-48
US-08-008-31-398A-48
                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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-09-293-533-66
-08-752-844-15
-08-591-196-15
                                                                                                                                                                                                                                                                                          572060 seqs, 82675679 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    - protein search, using sw model
                                                                                                    January 10, 2006, 20:34:27
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
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                                                                    OM protein
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No.
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Sequence 2. Application US/09192838B

Sequence 355244

GENERAL INFORMATION:
APPLICANT: POON, KENNECH A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
FILE REFREENCE: 30414200050
CURRENT APPLICATION NUMBER: US/09/192,838B
CURRENT FILING DATE: 1998-11-16
FRIOR APPLICATION NUMBER: 60/065,774
FRIOR PILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 5
SOFTHARE: PATENTING OF SEQ ID NOS: 5
SOFTHARE SET SECTION OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
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APPLICANT: THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
APPLICANT: THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
APPLICANT: CHATTERIEE, Malaya
APPLICANT: FOON, Kenneth A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
FILE REFERENCE: 304142000540
CURRENT FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: 60/065,774
EARLIER PILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VEY. 2.0
                                                  Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 34, Appli
Sequence 34, Appli
Sequence 34, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 27, Appli
Sequence 132, Appli
Sequence 132, Appli
Sequence 132, Appli
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Sequence 134, Appli
Sequence 4, Appli
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Sequence 3, Al
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US-08-331-397B-48
US-08-759-804A-48
US-09-227-633-48
US-09-227-633-48
US-09-657-274-3
PCT-US94-06687-3
US-08-331-398A-34
US-08-331-398A-34
US-08-331-397B-34
US-08-759-804A-34
US-08-053-171-9
US-10-226-795-27
US-10-226-795-27
US-09-217-268B-27
US-09-217-268B-27
US-09-217-268B-27
US-09-254-180C-183
US-09-254-180C-183
US-08-285-936-4
US-08-285-936-4
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US-09-324-191-2
; Sequence 2, Application US/09324191
; Patent No. 6562798
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Best Local Similarity 93.8
Matches 105; Conservative
     ORGANISM: Mus Musculus
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| US-08-152-844-56
| Patent No. 593581
| GENERAL INFORMATION:
| APPLICANT: Chatterjee, Malaya |
| APPLICANT: Chatterjee, Malaya |
| APPLICANT: Poon, Kenneth A. |
| APPLICANT: Chatterjee, Malaya |
| TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE |
| TITLE OF INVENTION: MERCHANIA OF MELANOMA AND SMALL CELL CARCINOMA |
| TITLE OF INVENTION: FORESTER |
| TITLE 
                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                          Length 149;
                                                                                                                                                                                                                  Query Match 93.4%; Score 551; DB 2; Length 14: Best Local Similarity 93.8%; Pred. No. 7.6e-46; Matches 105; Conservative 1; Mismatches 6; Indels
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FILING DATE:
FLING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCALIff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 3041:
TELECHONE: (415) 813-5600
TELECHONE: (415) 494-0792
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TELERAX: 706141
INFORMATION POR SEQ.
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
"VPE: amino acid
"'PE: amino acid
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Matches 105, Conservative
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MOLECULE TYPE: protein
                                                                      TYPE: PRT
COGANISM: Mus Musculus
US-09-324-191-2
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                                       LENGTH: 149
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SEQ ID NO 2
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152 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRF 211
RESULT 4

US-09-293-533-66

US-09-293-533-66

Sequence 66. Application US/09293533

Patent No. 6509016

GENERAL INFORMATION:

APPLICANT: Charterjee, Malaya

APPLICANT: Charterjee, Sunil K.

TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE

TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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US-08-752-844-15

Sequence 15, Application US/08752844

Sequence 15, Application US/08752844

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya

APPLICANT: Poon, Kenneth A.

APPLICANT: Chatterjee, Sunil K.

TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE

TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
SUFTREMY APPLICATION NATA:
APPLICATION NUMBER: US/09/293,533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
APPLICATION NUMBER: US/08/752,844
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERRENCE/DOCKET NUMBER: 30414-20002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 263 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-09-293-533-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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TELEX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CA
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                          US-08-591-196-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-293-533-15
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Sequence 15, Application US/08591196

Patent No. 5977316

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya

APPLICANT: Foon, Kenneth A.

TITLE OF INVENTION: TREATMENT OF MELANOMA AND USE FOR THE

TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FORESTER

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CA

COUNTY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER: Elopy disk

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATE:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/591,196

FILING DATE: 16-JAN-1996

SAPPLICATION NUMBER: US/ORDENT APPLICATION TAXEN-LOAD
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                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 92.9%; Score 548; DB 1;
Best Local Similarity 93.8%; Pred. No. 1.1e-45;
Matches 105; Conservative 1; Mismatches 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                          30414-20002.21
                                                                                                              ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ADDRESSE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUBER: 30414
TELECOMMULCATION INFORMATION:
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acids
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                                                                                                    USA
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1 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKKGQSPKLLIYFVSNRF 60
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Fatent No. 6509016
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Chatterjee, Malaya
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOWA AND SMALL CELL CARCINOWA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 92.9%; Score 548; DB 1; Length 112; Best Local Similarity 93.8%; Pred. No. 1.1e-45; Matches 105; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,533
                                                         30414-20002.20
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REPERNICE/DOCKET NUMBER: 3041
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 813-5600
TELEFAX: (415) 494-0792
TELEFAX: 706141
INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40, 253
REGISTRATION NUMBER: 40, 253
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELERAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 112 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08752844

Patent No. 5935821

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya

APPLICANT: Chatterjee

APPLICANT: Chatterjee

APPLICANT: Chatterjee

APPLICANT: Chatterjee

APPLICANT: Chatterjee

APPLICANT: Chatterjee

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                                                                                                                              Length 112;
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92.9%; Pred. No. 1.8e-45;
ive 1; Mismatches 7; Indels
                                                                                                                                                                                                          6; Indels
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STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/752,844
                                                                                                                      Score 548; DB 2;
Pred. No. 1.1e-45;
1; Mismatches 6;
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CLASSIFICATION: 424
ATTORNEY, AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REPERENCE/DOCKET NUMBER: 30414
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 813-5600
TELEFAX: (415) 494-0792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
                                                                                                                          92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 149 amino acids
amino acid
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Matches 104; Conservative
                                                                                                                                                                                                          Matches 105; Conservative
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MOLECULE TYPE: protein
MOLECULE TYPE: peptide
                                                                                                                          Query Match
Best Local Similarity
                ; MOLDECOLD ; US-09-293-533-15
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US-08-752-844-2
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RESULT 9

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20 DVFMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEMYLQKPGQSPNLLIYFVSNRF 79
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Sequence 2, Application US/08591196
Fatent No. 5977316
Fatent No. 5977316
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Chatterjee, Malaya
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: MRRISOW & FORESTER
STREET: 755 FAGE MILL ROAD
COMMENTION: COMMENTION OF MELANOMA AND SMALL CELL CARCINOMA
COMMENTED OF SEQUENCES: 57
CORRESPONDED OF SEQUENCES: 57
CORRESPONDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-293-533-2

Sequence 2, Application US/09293533

Sequence 2, Application US/09293533

Sequence 2, Application US/09293533

Patent No. 5630916

APPLICANT: Chatterjee, Malaya

APPLICANT: Foon, Kenneth A.

APPLICANT: Chatterjee, Sunil K.

TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE

TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FORESTER

STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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Pred. No. 1.8e-45;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
COUNTRY: USA
ZIP: 94304-1018
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYBE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,196
FILING DATE: 16-JAN-1996
CLASSIFICATION: 424
ATTORNEY/AGRY INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.20
TELECOMMUNICATION INFORMATION:
TELEFRANK: (415) 494-0792
TELEFRANK: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.7%;
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Best Local Similarity 92.9
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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STATE: Utah
COUNTRY: United States of America
TELECOMMUNICATION INFORMATION:
                                                        TELEX: 388961 1PMOUT
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
                                                                                                                                                                                                                                                                                                                n 92.4%;
Similarity 92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 amino acids
                       : 801/532-1922
801/531-9168
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Best Local Similarity 92.9
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                            Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                     TYPE: amino acid STRANDEDNESS: unb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                              ; HYPOTHETICAL:
US-08-497-312-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-560-558E-27
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                                                                                                                                                                                                    TOPOLOGY:
                                            TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 547; DB 2; Length 149;
Pred. No. 1.8e-45;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 11600
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,312
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 80/94
FILING DATE: 30-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOND, LAURENCE B.
                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,533
PLING DATE:
PLING DATE:
ATFORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/752,844
FILING DATE:
ATFORNEY/AGENT INFORMATION:
NAME: SCHAFF, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/POCKET NUMBER: 30414-20002.21
TELEPROWNICATION INFORMATION:
TELEPROWNICATION INFORMATION:
TELEPROWNICATION INFORMATION:
TELEPROWNICATION INFORMATION:
TELEPRAKE: (415) 813-5600
TELEFRAK: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Method for obtaining modification of INVENTION: immunoglobulins with reduce TITLE OF INVENTION: antibody variable domains, NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: CENTRO DE INMUNOLOGIA MOLECULAR STEET: 215 Y 15, ATABEY PLAYA
CITY: HAVANA
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30,549
ER: 2629US
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Patent No. 5712120
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 706141
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: IENGTH: 149 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 92.7%;
Best Local Similarity 92.9%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BOND, LAURENCE B.
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: CUBA
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Sequence 27, Application US/08560558E

Sequence 27, Application US/08560558E

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Humanized and chimeric monoclonal
TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor
TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor
TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor
TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor
TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor
TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor
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TITLE OF INVENTION: THAT RECOGNIZE epidermal growth factor receptor
TITLE OF INVENTION: THAT RECOGNIZE epidermal growth factor receptor
TITLE OF INVENTION: THAT RECOGNIZE epidermal growth factor receptor
TITLE OF INVENTION: THAT RECOGNIZE epidermal growth factor receptor recognized epidermal growth factor receptor receptor recognized epidermal growth factor receptor receptor receptor recognized epider
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            Length 113;
Score 545; DB 1; Length 11
Pred. No. 2.1e-45;
1; Mismatches 7; Indels
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ZIP: 84110
ZIP: 84110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPRATING SYSTEM: WINDOWS95
SOFTWARE: WORDERfect 5.1/5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,558E
FILING DATE: NO. 5891996ember 17, 1995
ATTORNEY/AGENT INFORMATION:
NAME: TULING DATE: A10.
REGISTRATION NUMBER: 33,041
REGISTRATION NUMBER: 2720US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 531-9168
TELEPHONE: (801) 531-9168
TELEPHONE: GROUN STATOS:
TELEPHONE: CHARACTERISTICS:
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61
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DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
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                                                                                                                                                                                                                                                                                                                                         APPLICANT: Williams. David
APPLICANT: FitzGerald, David
APPLICANT: FitzGerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
ADDRESSEE: Townsend and Townsend and Tareet Plaza
                                                                                                                         61 SGVPDRFRGSGSGTDFTLKISRVEAEDLGVYYCFQYSHVPWTFGGGTKLEIK 112
                                                                                                61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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MEDIUM TYPE: Plopy disk

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 09/331,398A

FILING DATE: 30-CT-1994

PRIOR APPLICATION NUMBER: US 07/767,331

PRIOR APPLICATION NUMBER: US 07/767,331

PRIOR APPLICATION NUMBER: US 07/596,289

FILING DATE: 12-CCT-1990

ATTORNEY/AGENT INFORMATION:

NAME: HUMLEY, TOWN

NAME: HUMLEY, TOWN

NAME: HUMLEY, TOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: One Market Plaza, Steuart Street Plaza CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   015280-126110US
                                                                                                                                                                                                                                                          Sequence 67, Application US/08331398A Patent No. 5608039 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                    Pastan, Ira
Willingham, Mark
FitzGerald, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 125 amino acids
amino acid
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MOLECULE TYPE: protein
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COCATION: 1..125
OTHER INFORMATION:
OTHER INFORMATION:
US-08-331-398A-67
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US-08-331-398A-67
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APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DVLLIQIPLSLPVSLGDQASISCRSSQSIVHSNGNIYLEWYLQKPQQSPKLLIXKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DVLATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
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61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPFTFGSGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Mouse monoclonal antibody B5
Light chain region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER TELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION NUMBER: US 07/767,331
PRIOR APPLICATION NUMBER: US 07/767,331
PRIOR APPLICATION NUMBER: US 07/767,331
PRIOR APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: HUMBER: 12-OCT-1990
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION NUMBER: 015280-126120US
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STRET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                Sequence 67, Application US/08331397B; Patent No. 5981726; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 125 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Region
LOCATION: 1..125
CHER INFORMATION: /
CTHER INFORMATION: US-08-331-3978-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
: USA
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                                                                                                      RESULT 14
US-08-331-397B-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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Under Statement 66, Application Us/08759804A

Sequence 66, Application Us/08759804A

Seriant No. 599236

SEREAL INFORMATION: 18.

APPLICANT: Pittedraid, buyed J.

APPLICANT: Provised and Townsend and Crew LiP

STREET: Two Smbarcadero Center, Eighth Floor

TALENGARFORTON SMBAR: Scottly Smbarcadero Center, Eighth Floor

TATION SMBARCAGERITON SMBAR: Scottly Smbarcadero Center, Eighth Floor

TATION SMBARCAGERITON SMBAR: Scottly Smbarcadero Center, Eighth Floor

TELECOMMITTION SMBAR: SMBARCAGERITON SMBARCAGEROUS CENTERORY CONCOUNTS CENTER SMBARCAGEROUS CENTERORY C
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Search completed: January 10, 2006, 20:58:02 Job time : 22.8706 secs

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January 10, 2006, 20:53:43; Search time 61.4328 Seconds (without alignments) 761.757 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                            590
1 DYLMTQIPLSLPVSLGDQAS......CFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA Main: *

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: *

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: *

4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: *

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: *

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: *

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep: *
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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                             Copyright
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		de			SUMMARIES		
Result No.	Score	Query Match	Length	DB	σι	Description	
-	590	100.0	112	2	US-10-735-916A-54	54,	
8	590	100.0	122	ហ	US-10-735-916A-49	Sequence 49, Appl	
e	564	92.6		m	US-09-995-529-10	10,	
4	564	95.6	112	m	US-09-995-529-10	2	
S	564	95.6		Ŋ	US-10-735-916A-56	26,	
y	558	94.6		4	US-10-258-728-4	4,	
7	553	93.7	112	4	US-10-258-728-25		
80	551	93.4		m	US-09-990-205-2	'n	
σ	551	93.4	263	4	US-10-153-401-66	99	
10	550	93.2		4	US-10-454-660-10	20,	
11	548	92.9	112	4	US-10-153-401-15	12	
12	547	92.7	112	വ	US-10-735-916A-57	2,	
13	547	92.7	113	Ŋ	US-10-729-441-69	69	
14	547	92.7		ഹ	US-10-897-406-69	69	
15	547	92.7		4	US-10-153-401-2	7	
16	547	92.7		9	US-11-093-103-84	84,	
17	545	92.4		'n	US-10-735-916A-55	22,	
18	545	92.4		S	US-10-828-782A-16	4	
19	544	92.2	113	ß	US-10-729-441-61	61,	
20	544	92.2		'n	US-10-897-406-61	61, 7	
21	544	92.2		4	US-10-803-622-190	190,	
22	544	92.2		4	US-10-803-653-190	190,	
23	543	92.0	114	9	US-11-009-443-29	29, 1	
24	542	91.9		4	US-10-434-469-43	43,	
25	542	91.9	112	ß	10-482-105-	4	
26	542	91.9		2	US-10-500-207A-6	ģ	
27	542	91.9	113	ß	US-10-729-441-60	Sequence 60, Appl	

80	542	6	113	ď	118-10-897-406-60	Sequence 60, Appl
6 6	542	91.9	131	4	US-10-434-469-6	9
30	542	91.9	131	Ŋ	US-10-482-105-4	Sequence 4, Appli
31	542	91.9	131	Ŋ	US-10-409-611-75	75,
32	542	91.9	131	'n	US-10-409-608A-17	17
33	542	91.9	131	Ŋ	US-10-500-207A-4	4,
34	541	91.7	113	Ŋ	US-10-729-441-59	29
35	541	91.7	113	S	US-10-897-406-59	5,0
36	541	91.7	114	9	US-11-009-443-75	75,
37	541	91.7	116	Ŋ	US-10-787-219A-49	4
38	540	91.5	131	4	US-10-388-214A-2	7
39	540	91.5	220	9	US-11-013-537-55	รร
4	539	91.4	149	4	US-10-226-795-27	27, 7
41	538	91.2	112	4	US-10-308-817-172	17
42	538	91.2	112	4	US-10-308-817-181	181,
43	538	91.2	112	4	US-10-453-698-172	172,
44	538	91.2	112	Ŋ	US-10-735-916A-61	61, A
45	538	91.2	114	m	US-09-217-268B-27	27,
					ALIGNMENTS	
1 11000						
US-10-735-916A-54	-916A-	54				
; Sequence	t 54,	Sequence 54, Application US/10735916A	ion US	710	735916A 1	
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ö 9 1 DVIANTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIXKVSNRL 60 1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL Gaps GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: US/30/216
FRIOR APPLICATION NUMBER: PC 03/08 538
FRIOR APPLICATION NUMBER: FR 03/08 653
FRIOR APPLICATION NUMBER: FR 02/00 653
FRIOR APPLICATION NUMBER: FR 02/00 654
FRIOR APPLICATION NUMBER: FR 02/05 654
FRIOR PILING DATE: 2002-01-18
FRIOR PILING DATE: 2002-01-18
FRIOR PILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTIN VOIC: 2.1 ; 0 Length 112; Indels . 0 Query Match
100.0%; Score 590; DB 5;
Best Local Similarity 100.0%; Pred. No. 3.4e-49;
Matches 112; Conservative 0; Mismatches 0; ; ORGANISM: Mus musculus US-10-735-916A-54 g ઠ ò g

RESULT 2 US-10-735-916A-49

S-10-735-916A-49 Sequence 49, Application US/10735916A Publication No. US20050084906A1

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1 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FULLICACION NO. USZUUJOUB4906A1
GENERAL INFORMATION:
APPLICANT: GOETSCH, Liliane
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: HECK, Alain
APPLICANT: HELW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REPERENCE: 0.7753-183
CURRENT APPLICATION NUMBER: W6 03-12-16
FRIOR PILING DATE: 2003-07-11
FRIOR PILING DATE: 2003-07-11
FRIOR PILING DATE: 2003-01-18
FRIOR PILING DATE: 2002-01-18
FRIOR PILING DATE: 2002-01-18
FRIOR PILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR APPLICATION NUMBER: FR 02/06 554
FRIOR FILING DATE: 2002-05-07
FRIOR APPLICATION NUMBER: FR 02/05 753
61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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Pred. No. 1.1e-46;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                           Sequence 10, Application US/09995529

Fublication No. US20040091482A9

GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Related Methods
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358

SEQ ID NO 10

SEQ ID NO 10

LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 564; DB 3;
Pred. No. 1.1e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 56, Application US/10735916A Publication No. US20050084906A1
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95.5<del>%</del>;
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Best Local Similarity 95.5%;
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Mus musculus
US-09-995-529-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus
US-10-735-916A-56
                                                                                                                  US-09-995-529-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                    APPLICANT: GORNALA, Nathalie
APPLICANT: GORNALA, Nathalie
APPLICANT: DEGER, Olivier
APPLICANT: DEGER, Olivier
APPLICANT: DEGER, Alain
APPLICANT: DEGER, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: PR 03/08 538
PRIOR APPLICATION NUMBER: PR 03/08 538
PRIOR PLING DATE: 2003-01-10
PRIOR PLING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR PLING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/05 553
PRIOR PLING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/05 553
PRIOR APPLICATION NUMBER: FR 02/05 553
PRIOR PLING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTIN Ver. 2.1
LENGTH: 122
TWONE: DDT
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Pred. No. 1.1e-46;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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Sequence 10, Application US/09995529

Publication No. US20030099655A1

GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Related Methods
TITLE OF INVENTION: Related Methods
CURRENT APPLICATION WUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 112
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Best Local Similarity 100.0%; Pred. No. 3.7e-49;
Matches 112; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 95.5%;
Matches 107; Conservative
                              APPLICANT: GOETSCH, Liliane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Mus musculus US-09-995-529-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Mus musculus
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Gaps

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Gaps

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Sequence 2, Application US/09990205;
Sequence 2, Application US/09990205;
Patent No. US20020150572A1
GENERAL INFORMATION:
APPLICANT: FOON, Kenneth A.
APPLICANT: FOON, Kenneth A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
FILE REFERENCE: 304142000501
CURRENT APPLICATION NUMBER: US.09/990,205
CURRENT FILING DATE: 2001-11-20
PRIOR FILING DATE: 1998-11-16
PRIOR FILING DATE: 1998-11-16
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVIATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
                            1 DVIAMIQTPLSLPVSLGDQASASCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIXKVSNRF 60
1 DVLATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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                                                                                                                 61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGIYYCFQGSHVPWTFGGGTKLEI
                                                                                         61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 93.4%; Score 551; DB 3; Length 149; Best Local Similarity 93.8%; Pred. No. 2.7e-45; Matches 105; Conservative 1; Mismatches 6; Indels
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CUNTRY: USA

CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,401
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: MORLISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
COGGANISM: Mus Musculus
US-09-990-205-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 149
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Sequence 4, Application US/10258728

Publication No. US20040091485A1

GENERAL INFORMATION:

APPLICANT: Ellis, John Robert Maxwell

APPLICANT: Ellis, John Robert Maxwell

TITLE OF INVENTION: Humanised Antibodies to the Epidermal Growth Factor Receptor

FILE REFERENCE: 28438-1010501

CURRENT FILING DATE: 2003-06-18

PRIOR APPLICATION NUMBER: GB 0011981.8

PRIOR APPLICATION NUMBER: GB 0011981.8

PRIOR APPLICATION NUMBER: GB 0020794.4

PRIOR FILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTHER: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-258-728-25

Sequence 25, Application US/10258728

Sequence 25, Application No. US20040091485A1

Publication No. US20040091485A1

GENERAL INFORMATION:

APPLICANT: Blis, John Robert Maxwell

APPLICANT: Durrant, Linda Gillian

TILE REFERENCE: 28438-101US01

CURRENT APPLICATION WUMBER: US/10/258,728

CURRENT APPLICATION WUMBER: GB 0011981.8

PRIOR FILING DATE: 2000-05-19

PRIOR APPLICATION WUMBER: GB 0020794.4

PRIOR APPLICATION NUMBER: GB 020794.4

PRIOR APPLICATION NUMBER: 2000-08-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.1

LENGTH: 112
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                            1 DVIANTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKILIYKVSNRL 60
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                                                                                                                 61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                         61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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CRGANISM: Mus musculus
US-10-258-728-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Mus musculus
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61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCPQGSHVPYTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
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Sequence 10, Application Wolfout School Sequence 10, Publication No. US20040005550A1

GENERAL INFORMATION:
APPLICANT: Shattil, Sanford J.
APPLICANT: Hato, Taka
APPLICANT: Hato, Taka
APPLICANT: Stupack, Dwayne
APPLICANT: Stupack, Dwayne
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR TARGETING
TITLE OF INVENTION: ACTIVATED VITRONECTIN RECEPTOR ALPHA V BETA 3
FILE REPERBNCE: NOV0149S
CURRENT APPLICATION NUMBER: US/10/454,660
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/454,925A
PRIOR APPLICATION DATE: 1999-12-03

PRIOR APPLICATION NUMBER: PRIOR APPLICATOIN NUMBER: US/09/454,925A

WINDER OF AT A WARNEY OF A
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US-10-454-660-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.4%; Score 551; DB 4; Length 263; 93.8%; Pred. No. 5e-45; tive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 219;
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                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Catherine M. Polizzi
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
                                               FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
                                                                                                                                                                       APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
        APPLICATION NUMBER: US 09/293,533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 263 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 706141
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarica
Matches 105; Conservative
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LENGTH: 219
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                                                                                                         Foon, Kenneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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Pred. No. 3.8e-45;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORPUTER: ISE FLORY ULSE.

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,401
FILING DATE: 27-Aug-2002
CLASSIFICATION: VUNKNOWN>
PRIOR APPLICATION OF VONCHOWNS
PRIOR APPLICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1995-01-16
ATTORNEY/AGENT INFORMATION:
NAME: Cacherine M. Polizzi
RESISTRATION NUMBER: 40,130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 304142000202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-10-735-916A-57
Sequence 57, Application US/10735916A
; Publication No. US20050084906A1
                 ; Sequence 15, Application US/10153401
; Publication No. US20030114398A1
; GENERAL INFORMATION:
                                                                                            APPLICANT: Chatterjee, Malaya
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.9%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304-1018
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Best Local Similarity
US-10-153-401-15
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Best Local Similarity
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US-10-153-401-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
        GENERAL INFORMATION:

APPLICANT: GORTSCH, Liliane
APPLICANT: CORVALA, Nathalie
APPLICANT: CORVALA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: DUFLOS, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: ONOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: PR 03/08 538
PRIOR PELING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PR 02/00 653
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 57
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YGVPDRFSGSGSGTDFTLKISSVRAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGTHVPYTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 69, Application US/10729441
| Publication No. US20040265307A1
| GENERAL INFORMATION:
| APPLICANT: ImmunoGen, Inc.
| TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
| FILLE REFERENCE: A6689
| CURRENT FILLING DATE: 2003-12-08
| PRIOR PPLICATION NUMBER: 10/170,390
| PRIOR FILING DATE: 2002-06-14
| NUMBER OF SEQ ID NOS: 96
| SEQ ID NO 69
| LENGTH: 113
| TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 547; DB 5;
Pred. No. 4.8e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (28)...(28)
OTHER INFORMATION: "X" may be any amino acid
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LOCATION: (101)..(101)
OTHER INFORMATION: "X" may be any amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 92.0%;
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Mus musculus
US-10-735-916A-57
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92.7%; Score 547; DB 5; Length 113;

Query Match

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Publication No. US20030114398A1
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
Foon, Kenneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: TREATMENT OF MELANOMA AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                              1 DVLATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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                         0; Gaps
                                                                                                                                                                                61 YGVPDRPSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                  61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCPQGSHVPXTPGGGTKLEIK 112
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93.8%; Pred. No. 4.8e-45;
iive 1; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                            Sequence 69, Application US/10897406
Publication No. US20050186203A1
GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILE REFERENCE: A8338
CURRENT APPLICATION NUMBER: US/10/897,406
CURRENT APPLICATION NUMBER: US/10/170,390
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin version 3.1
SEQ ID NO 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
92.7%; Score 547; DB 5; I
Best Local Similarity 93.8%; Pred. No. 4.8e-45;
Matches 105; Conservative 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: synthetic antibody structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (28)...(28)
OTHER INFORMATION: "X" may be any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC FEATURE
1 LOCATION: (101)...(101)
2 OTHER INFORMATION: "X" may be any amino acid
US-10-897-406-69
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CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                            Conservative
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COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: HEM PC compatible

COMPUTER: HEM PC compatible

COMPUTER: HEM PC compatible

COMPUTER: HEM PC compatible

COMPUTER: HEM PC COMPUTER: HEM PC COMPUTER:

COMPUTER: HEM PC COMPUTER: HEM PC COMPUTER:

FILING DATE: 1-202

FILING DATE: 1-202

FILING DATE: 1-202

FILING DATE: 1-203

FILING DA
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Search completed: January 10, 2006, 21:35:30 Job time : 62.4328 sec8

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January 10, 2006, 20:07:41; Search time 77.3134 Seconds (without alignments) 636.505 Million cell updates/sec
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1 DVLMTQIPLSLPVSLGDQAS......CPQGSHVPWTFGGGTKLEIK 112
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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                     2443163 seqs, 439378781 residues
                                                                                                                                                                                                                                                                                                                                                                                          summaries
                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 su
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seg length: 200000000
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Sequence:
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Maximum DB 8
                                                           OM protein
                                                                                                                                                                                                                                                        Searched:
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                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adj76888 Anti-IGF-	Adz67058 Murine im	Adj76883 Anti-IGF-	Adz67053 Murine im		Adj76890 Anti-IGF-	Adz67060 Mouse ant	Aae15704 Mouse mon	Aeb21358 Mouse ant	Aeb31116 Antibody	Adi26498 Human ECL		Adp84941 Variable	Aec21825 Mouse lig	Ads88785 Seguence	Adp84942 Variable	Aap80154 Biosynthe		Aay21545 Monoclona	Aay28470 Vh-(Lk)-V	Ada14828 Anti-idio	Adc35357 Monoclona		Aap81364 Light cha
SUMMARIES	ΙD	ADJ76888	ADZ67058	ADJ76883	ADZ67053	ADD94125	ADJ76890	ADZ67060	AAE15704	AEB21358	AEB31116	ADI26498	ADI26490	ADP84941	AEC21825	ADS88785	ADP84942	AAP80154	AAW03199	AAY21545	AAY28470	ADA14828	ADC35357	ADS88781	AAP81364
	DB	7	σ	~	σ	7	7	σ	ഹ	თ	σ	œ	œ	œ	σ	œ	œ	-	~	~	~	9	7	۵	Н
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de	Query Match	100.0	100.0	100.0	100.0	92.6	92.6	92.6	94.6	94.6	94.6	94.2	94.1	94.1	94.1	94.1	93.7	93.6	93.4	93.4	93.4	93.4	93.4	93.2	93.2
	Score	590	590	590	590	564	564	564	558	558	558	556	555	555	555	555	553	552	551	551	551	551	551	550	550
	Result No.	1	7	m	4	ß	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Aab62301 Chimeric Aav95258 WOW-1 Fab			_	7		Adp84938 Variable	Adp84966 Murine an		4 Single		N	Adp84961 Single ch	Adp84960 Single ch	ø	8 Single	a)	6 Single	5 Sing	Adp84954 Single ch
AAB62301 AAY95258	ADS88777	ABP52310	AAY49217	ADA14777	ADC35319	ADP84938	ADP84966	ADP84971	ADP84964	ADP84963	ADP84962	ADP84961	ADP84960	ADP84959	ADP84958	ADP84957	ADP84956	ADP84955	ADP84954
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115	298	109	112	112	112	114	219	219	257	258	259	260	261	262	263	264	265	266	267
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550	550	549	548	548	548	548	548	548	548	548	548	548	548	548	548	548	548	548	548
25	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ADJ76888 standard; protein; 112 AA

(first entry)

06-MAY-2004

ADJ76888;

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or-2; and/or (i) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers. Disclosure; SEQ ID NO 54; 164pp; French. cytostatic; antipsoriatic; antibody; (FABR) FABRE MEDICAMENT SA PIERRE. Leger O; Anti-IGF-1R related protein #5. 18-JAN-2002; 2002FR-0000653. 18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-00005753. 20-JAN-2003; 2003WO-FR000178. Corvaia N, WPI; 2003-569653/53 WO2003059951-A2. Mus musculus. 24-JUL-2003. Goetsch L,

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          transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate. Jung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immune disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin light chain variable region 7C10 VL SEQ ID NO:54.
                                                                                                                                                                                                         DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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                                                                                                                                               Length 112;
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these receptors with their ligands. Especially they inhibit
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                                                                                                                                              Score 590; DB 7;
Pred. No. 1.2e-45;
                                                                                                                                100.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         ADZ67058 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leger 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 2002FR-0000653.
; 2002FR-0000654.
; 2002FR-00005753.
; 2003WO-FR000178.
; 2003FR-00008538.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                             Matches 112; Conservative
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                                                                                                                                                               Local Similarity
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CORVAIA N.
LEGER O.
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                                                                                                                   Sequence 112 AA;
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18-JAN-2002;
07-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                    ADZ67058;
                                                                                                                                               Query Match
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(LEGE/)
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(HAEU/)
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Treeperor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting trowner kinase activity of the receptor.

Comprision a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGRF, and/or connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGRF, and/or connected with an overexpression and/or an abnormal contractivation of the transduction pathway of the signal mediated by the interaction of IGF or IGF2 with IGF-IR and/or or EGRF with EGRF, where the administration of the medicament does not induce or only sightly interaction of the transformation of normal cells into cells with tumoral creature, preferably IGF-dependent, especially IGF and/or IGF2.

Consistent intended for preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent and/or EGF-dependent of medicament intended for prevention or for the treatment of encer is chosen from prostate cancer. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer. (I) is useful in the preparation of a medicament intended for the specific targeting of a biologically active compound to the specific targeting of a biologically active compound to cells expressing or overexpressing of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor. (I) a useful for in vitro diagnosis of illnesses induced be abnormed to be additio
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invention relates to a novel isolated anti-insulin-like growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGOSPKLLIYKVSNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ76883 standard; protein; 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-IGF-1R related protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 112 AA;
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or retar diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (IGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Bspecially they inhibit transformation of normal cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis, ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 49; 164pp; French
                                                                                                                                                                                                                                                          (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                  Leger O;
20-JAN-2003; 2003WO-FR000178
                                                                              18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                                                                                                                  Corvaia N,
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100.0%; Score 590; DB 7; Length 122; 100.0%; Pred. No. 1.3e-45; tive 0; Mismatches 0; Indels 0 Matches 112; Conservative Local Similarity Query Match #X###X#X#X#X#X##X

DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL н 11

61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 122

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ADZ67053 standard; protein; 122 AA ADZ67053

(first entry) 30-JUN-2005

Murine

immunoglobulin light chain variable region 7C10 VL SEQ ID NO:49.

Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lump tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; light chain variable region.

Mus musculus

'note= "leader peptide" Location/Qualifiers /note= "CDR1" 49 Peptide Region THE LEFT SON THE STATE OF THE S

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Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) artibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Leger O, Duflos A, Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 8; SEQ ID NO 49; 125pp; English.
65. .71
/note= "CDR2"
                                                                                                                                                                                                                18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                    /note= "CDR3"
                                                                                                                                                                16-DEC-2003; 2003US-00735916
                                                                                                                                                                                                    2002FR-00000653
                                  104. .111
                                                                                                                                                                                                                                                                                                                                                                                                                                               Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-321968/33.
                                                                                                                                                                                                                                                                                                              GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                    DUFLOS A. HAEUW J.
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                                                                                          US2005084906-A1
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Gaps

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The invention relates to a novel isolated anti-insulin-like growth factor.

Treceptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of expeditionally inhibiting try triase activity of the receptor, comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary capable (GR) consisting of one of two fully defined is amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of activation of the IGF-IR and/or EGFR, and/or connected with a hyperactivation of the ransduction pathway of the signal mediated by the interaction of IGF-IR and/or EGFR, and/or of IGFI and/or IGF2—connected with inhibition of the insulin contracter, preferably IGF-dependent, especially IGF1 and/or IGF2—copendent, and/or EGFR-dependent and/or EGFR-dependent and/or HER2/neu-dependent and/or IGF2-dependent and/or EGF-dependent of tumor calls, preferably IGF-and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent of tumor calls, preferably IGF-and/or IGF2-dependent and/or EGF-dependent calls (I) is useful in the preparation of a medicament intended for the proliferation of a medicament intended for the proliferation of a medicament intended for the prevention or of the preparation of a medicament intended for the prevention or of the preparation of a medicament intended for the prevention o overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.

122 AA; Sequence

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Gaps

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4; Indels

Mismatches

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107; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment comprising one or more complementarity determining regions cides of a defined light CDR and a heavy CDR with at least one amino acid (as) substitution where the antibody has specific binding activity for a cryptic collagen epitope. The growth of all solid tumours requires new blood vessel growth, anglogenesis, inhibition of which is an approach to limiting tumour growth. The invention may allow development of therapeutics with a cytostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with anglogenesis, tumour growth and/or cancer metastasis. The present sequence is the partial amino acid sequence of the mouse anticryptic collagen site antibody HU177 variable region light chain used during the creation of the antibody of the invention.
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                                                                            DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                                                                                                                                            grafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth; angiogenesis; tumour growth; cytostatic; collagen antigonist; cancer metastasis; anti-cryptic collagen; antibody; HUI77; variable region light chain; mouse; murine.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a novel grafted antibody or its functional
                                                                                                                                                                                                                                                                        Mouse HUI77 variable region light chain partial amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.
                                                                                                             61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                          YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFOGSHVPWTFGGGTKLEIK 122
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              Length 122;
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                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Broek D, Brooks PC;
            Score 590; DB 9;
Pred. No. 1.3e-45;
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Pred. No. 2.6e-43;
100.0%; Scor...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                ADD94125 standard; protein; 112 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.6%;
95.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-NOV-2001; 2001US-00995529.
06-DEC-2001; 2001US-00011250.
                                                                                                                                                                                                                                                 (first entry)
                                     Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-513649/48.
N-PSDB; ADD94124.
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Best Local Similarity
                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           WO2003046204-A2
                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus.
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            Query Match
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or creat diseases associated with overexpression and/or abnormal activity of IGF-IR. Ab and its fragments are used to prevent or IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                             1 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF
DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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                                                                                                                                               61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                    SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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Pred. No. 2.6e-43;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 56; 164pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-IGF-1R related protein #7.
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
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Best Local Similarity 95.5%;
Matches 107; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-569653/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003059951-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                    RESULT 6
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGP-IR) antibody (I) or its functional fragment, being capable of bindding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor. Comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of the preparation of the IGP-IR and/or EGF, and/or connected with a noverexpression and/or an abnormal activation of the IGR-IR and/or EGF, and/or connected with a chyperactivation of the transduction pathway of the signal mediated by the interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended
                                                                                                                                                                                                                                                                                                                        Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; light chain variable region.
antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
                                                       61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                            SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beck A;
                                                                                                                                                                                                                                                                                        Mouse antibody light chain variable region SEQ ID NO:56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 12; SEQ ID NO 56; 125pp; English.
                                                                                                                                                                                  ADZ67060 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leger O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002FR-0000653.
2002FR-0000654.
2002FR-0005753.
2003WO-FR000178.
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                                                                                                                                                                                                                                                   (first entry)
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CORVAIA N.
LEGER O.
DUFLOS A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2002;
18-JAN-2002;
07-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                     30-JUN-2005
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(BECK/)
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(LEGE/)
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                                                                                                                                                             ADZ67060
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cc to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2-
Cdependent and/or EGF-dependent and/or HER2/new dependent calls. (I) is 
cuseful for preparation of a medicament intended to inhibit the growth 
and/or the proliferation of tumor cells, preferably IGF-dependent, 
EREZ/new dependent cells. (I) is useful in the preparation of a 
medicament intended for prevention or for the treatment of cancer, 
the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, 
the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, 
cc breast cancer, endometrial cancer or colon cancer. (I) is useful in the 
preparation of a medicament intended for the prevention or for the 
creatment of psoriasis. (I) is useful in preparation of a medicament 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; humanised form; monoclonal antibody alpha 340; gene therapy; epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast gastric; ovarian; immune response; cytostatic; cell growth; apoptosis; inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DVIAMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse monoclonal antibody alpha 340 light chain variable (VK) region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.6%; Score 564; DB 9; Length 112; 95.5%; Pred. No. 2.6e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE15704 standard; protein; 112 AA.
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24-AUG-2000; 2000GB-00020794.
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/label= CDR2
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|abel= CDR1
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/label= CDR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 112 AA;
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The present invention relates to a humanised form of the antibody 340 (a mouse monoclonal antibody which binds to epidermal growth factor (BGF) receptor and inhibits binding of BGF), obtainable from the cell line deposited with the BCACC under accession number 97021428. The humanised form of the antibody 340 is useful in gene therapy, medicine and in the manufacture of a medicament for treatment or prophylaxis of cancer. The manufacture of a medicament for treatment or prophylaxis of cancer. The invention is useful for treating colorectal, lung, breast, gastric or ovarian cancers or also for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing a protective immune response against cancer by optimised immunisation schedules. The humanised form of the antibody 340 has reduced immunogenicity but shows similar binding to cells expressing EGF receptor, as the original muxine antibody and has increased ability to receptor, as the original muxine antibody and has increased ability to inhibit the growth of EGF receptor expressing cells. The invention is used as cell growth and apoptosis inhibitor. The present sequence is mouse monoclonal antibody alpha 340 light chain variable (VK) region
                                                                                                                                                                                                New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer.
                                                                                                                                                                                                                                                                                                                       Claim 6; Fig 2; 53pp; English.
                                                           Ellis JRM, Durrant LG;
(SCAN-) SCANCELL LTD.
                                                                                                                   WPI; 2002-062384/08.
                                                                                                                                              N-PSDB; AAD25247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 112 AA;
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9 8 1 DVLATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 1 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 0; Gaps 61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEI 111 SGVPDRFSGSGSGTDFTLKISRVBAEDLGIYYCFQGSHVPWTFGGGTKLEI 111 Length 112; 4; Indels 94.6%; Score 558; DB 5; 94.6%; Pred. No. 9.1e-43; ive 2; Mismatches 4; Matches 105; Conservative Query Match Best Local Similarity d Š

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Interleukin-13; IL-13; antibody engineering; humanized antibody; Antiasthmaticf, Antiallergic; Permatory; Dermatological; Antiallergic; Respiratory-Gen.; Antiulcer, Gastrointestinal-Gen.; Ophthalmological; Osteopathic; Virucide; asthma; allergic rhinitis; atopic dermatitis;
                                                                                                                               Mouse anti-IL-13 antibody 227-26 light chain variable region (VX)
                                                                                                                                                                                                                               allergic conjunctivitis; eczema, urticaria; allergy;
chronic obstructive pulmonary disease; ulcerative colitis;
respiratory syncytial virus infection; uveitis; scleroderma;
osteoporosis; monoclonal antibody; light chain variable region.
                              AEB21358 standard; protein; 114 AA
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                  WO2005062967-A2.
                                                                                                22-SEP-2005
                                                                 AEB21358;
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RESULT 9
AEB21358
                                BXAXBXBXBXAAAAXXBXBXBXAXB
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Gaps

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Length 114; 4; Indels

Score 558; DB 9; Pred. No. 9.3e-43; 1; Mismatches 4;

94.6%;

Conservative

Matches 107;

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> 23-DEC-2004; 2004WO-US043501. 23-DEC-2003; 2003US-0532130P.

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Local

Query Match

Similarity

9

1 DVLATOTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRF 60

SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGGGTKLEIK 112 61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112

1 DVLATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL

The invention relates to an antibody or its antigen-binding fragment that binds by a precifically and with high affinity to glycosylated and non-binds appecifically and with high affinity to glycosylated and non-colling appecifically and with high affinity to glycosylated and non-colling appecifically and with high affinity to glycosylated and mouse II-13, and neutralizes human II-13 activity at an approximate molar ratio of 1:2 (Wabitili). Also included are an antibody that binds to the same epitope as the antibody of the light and heavy chain variable regions of the novel antibody, a hybridoma cell line that produces a monoclonal antibody cregions derived from 2288/C1, 2288-4, 227-26, and 227-43 and designated with the ArCC deposit number PrA-5657, PRA-5656, PRA-5654, and PRA-5655, crespectively), a cell line comprising the mucleic acid encoding the antibody a vector comprising the mucleic acid encoding the antibody, a composition (comprising the antibody and a physiologically acceptable cartier dilutent, extigient, or stabilizer), a variable light chain comprising an amino acid sequence having the formula: FRIA-CDRIZ-FRIJ-C New antibody or its antigen-binding fragment that binds specifically and with high affinity to glycosylated and non-glycosylated human interleukin-13 (IL-13), useful for treating IL-13-mediated disorders, such as asthma allergic rhinitis, atopic dermatitis, allergic conjunctivitis, eczema, utticaria, food allergies, chronic obstructive pulmonary disease, ulcerative colitis, RSV infection, uveitis, scleroderma, or osteoporosis. The present sequence represents a the light chain variable region of a ä Huang Singh S, Claim 10; SEQ ID NO 7; 129pp; English. mouse anti-IL-13 monoclonal antibody. Yan C, Σ Ξ WPI; 2005-506603/51. (TANO-) TANOX INC. Sequence 114 AA; and eczema. SC, Fung

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expresses and/or binds interleakin-13 (IL-13). The method comprises administering an anti-IL-13 antibody or its binding fragment that binds deministering an anti-IL-13 antibody or its binding fragment that binds expresses and/or binds interleakin-13 (IL-13). The method comprises administering and non-glycosylated and non-glycosylated and non-glycosylated man in-13, and neutralizes human IL-13 activity at an approximate molar ratio of 1:2 (Mab:IL-13). The method also describes 1) a method for treating Hodghin's disease comprisisng administering a daministering the antibody or binding fragment that comprising administering the antibody, or a binding fragment that chaption in thibiting IL-13 dependent proliferation of neoplastic cells in a mammal comprising administering the antibody or a binding fragment that cinhibits the biological activity of IL-13 and 3) diagnosing a cancer or tumor overexpressing IL-13 comprising the use of the anti-IL-13 antibody to detect overexpression of IL-13 in the biological sample taken from a patient suspected of having the cancer or tumor. The antibodies used in the method of the invention are 228B/C produced by the hybridoma designated PTA-565. The antibody is a human content of method of the hybridoma designated PTA-565. The antibody of a bunding content of enimations. The antibody, a single domain antibody and humanized antibody a single domain antibody will produced by the hybridoma designated cytotoxicity and or comprises a physiologically acceptable carrier, diluent, excipient, or stabilizer. The antibody mediates killing by antibody dependent cell-mediated cytotoxicity and/or complement cell-mediated cytotoxicity and or comprises at least a variable light or heavy chain region. The variable light or heavy chain region. The constant region further comprises a constant region. The constant region is from a region further comprises a constant region. The constant region is from an igg antibody. The antibody further comprises the heavy chain. The constant region is from an igg a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating a neoplasm, e.g. Hodgkin's disease, that expresses and/or binds interleukin-13 (IL-13) comprises administering an anti-IL-13 antibody or its binding fragment that binds to both glycosylated and non-glycosylated
                                                                                                                                                                                                                                                             cytostatic; antibody therapy; neoplasm; interleukin 13; IL-13; cancer; diagnosis; tumor; humanized antibody; cell proliferation; Hodgkins disease; cytotoxin; chemotherapy; lymphoma; skin tumor; stomach tumor; colon tumor; breast tumor; pancreatic tumor; liver tumor; prostate tumor; lung tumor; head and neck tumor; renal tumor; lung squamous cell carcinoma; brain tumor; Raposis carcinoma; solid tumor; monoclonal antibody; 227-26; 227-26-1; light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel method for treating a neoplasm that
                                                                                                                                                                                                              Antibody 227-26/227-26.1 variable light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; SEQ ID NO 7; 98pp; English.
                                                  AEB31116 standard; protein; 114 AA.
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                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moyle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2005062972-A2
                                                                                                                                                         22-SEP-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human IL-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus sp.
Synthetic.
                                                                                                    AEB31116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al antibody enzymes by identification of a catalytic n the stereostructure for production of antibody enzymes therapeutic agents for cancer and infectious diseases
associated with a cytotoxic agent, such as a radioisotope or a chemotherapeutic agent. The methods and antibodies are useful for traating neoplasms such as Hodgkin's lymphoma, skin cancer, stomach cancer, colon cancer, breast cancer, pancreatic cancer, liver cancer, prostate cancer, lung cancer, head-and-neck cancer, renal cell cancer, aguanous cell carrionan, AIDS-associated Kaposi's carcinoma and brain cancer. This sequence represents the humanized mouse monoclonal antibody 227-26 and 227-26 at variable light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVPDRFSGSGSGTDFTLKISRVEABDLGVYYCFQGSHVPYTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody; enzyme; virucide; anti-HIV; cytostatic; antibacterial; helicobacter pylori urease inhibitor; chemokine receptor CCR-5 antagonist; cancer; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                 Score 558; DB 9; Length 114;
Pred. No. 9.3e-43;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening potential antibody enzymes by triplet residue in the stereostructure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI26498 standard; protein; 114 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori; HIV; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ECL2B-4-L SEQ ID NO:34.
                                                                                                                                                                                                                                                                                                                                             94.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUL-2003; 2003WO-JP009147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002JP-00211768.
2003JP-00051943.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as diagnostic and therapincluding HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-132963/13.
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADI26499
                                                                                                                                                                                                                                                                                    Sequence 114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-FEB-2003;
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       by the method of the invention has virucide, anti-HIV, cytostatic, and antibacterial activity. The enzyme acts as a helicobacter pylori urease inhibitor, or chemokine receptor CCR-5 (HIV target) antagonist. The method of the invention is useful for the treatment, prevention and diagnosis of cancer and infectious diseases, especially infection by Helicobacter pylori or HIV. The present sequence is used in the exemplification of the invention.
produced
                                                                                                                                                                                                       1 DVLATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                       61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCPQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                    SGVPDRFSGSGSGTDFTLKISRVETEDLGVYYCFQGSHVPWTFGGGTKLRIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                       antibody; enzyme; virucide; anti-HIV; cytostatic; antibacterial; helicobacter pylori urease inhibitor; chemokine receptor CCR-5 antagonist; cancer; infectious disease; Helicobacter pylori; HIV; human.
are located sterically close to one another. An enzyme
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                                                                                                                                     Length 114;
                                                                                                                     Score 556; DB 8; Length 1.2. Pred. No. 1.4e-42;
                                                                                                                                                             1; Mismatches
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                                                                                                                                                                                                                                                                                                                          ADI26490 standard; protein; 114 AA
                                                                                                                                  94.2%;
93.8%;
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2003JP-00051943.
2003JP-00198270.
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17-JUL-2003; 2003JP-00198292.
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                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                             Matches 105; Conservative
                                                                                                                                                Local Similarity
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                                                                                                              Sequence 114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
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Screening potential antibody enzymes by identification of a catalytic triplet residue in the stereostructure for production of antibody enzymes as diagnostic and therapeutic agents for cancer and infectious diseases including HIV infection.

WPI; 2004-132963/13.

N-PSDB; ADI26491

Claim 39; SEQ ID NO 26; 232pp; Japanese.

The invention relates to a novel method for producing antibody enzymes comprising a structural analysis step which confirms the existence in the predicted stereostructure of the antibody based on its amino acid sequence of a catalytic triplet residue structure in which a serine residue, an aspartic acid residue, and a histidine or glutamic acid

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recognition molecules, e.g. antibodies (and nucleic acids) that bind specifically to Core-1 antigens, useful for diagnosis, treatment and prevention of tumors and metastases.
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residue are located sterically close to one another. An enzyme produced by the method of the invention has virucide, anti-HIV, cytostatic, and antibacterial activity. The enzyme acts as a helicobacter pylori urease inhibitor, or chemokine receptor CCR-5 (HIV target) antagonist. The method of the invention is useful for the treatment, prevention and diagnosis of cancer and infectious diseases, especially infection by Helicobacter pylori or HIV. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody; Core-1 antigen; framework region; immunoglobulin superfamily; protease inhibitor; lectin; helix-bundle protein; lipocalin; variable heavy chain; VI; varcine; diagnosis; alleviation; treatment; tumour; breast; colon; stomach; pancreas; large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
                                                                                                                                                                                                                                                                                                               1 DVLATQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                           1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                  61 YGVPDRFSGSGGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                          SGVPDRFSGSGSGTDFTLKINRVAAEDLGVYYCPQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel recognition molecules, especially
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                                                                                                                                                                                                                Length 114;
                                                                                                                                                                                                              94.1%; Score 555; DB 8; Length 11
93.8%; Pred. No. 1.7e-42;
tive 2; Mismatches 5; IndelB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Karsten U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP84941 standard; protein; 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2003; 2003WO-DE003994
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                                                                                                                                                                                                                                                      Matches 105; Conservative
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                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                           Sequence 114 AA;
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ADP84941
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lysine-rich region and/or a multimerisation domain, most particularly it is a single-chain antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment with peptide or protein, and/or an ig of types G, M, A, E or D and/or their subclasses. It may be human, additional sequences/structures in the constructs are ig domains of additional sequences/structures in the constructs are ig domains of various species, interacting or stabilising domains, signal sequences, tluorescent dyes, toxins, antibodies with catalytic activity or other specificities, cytolytic agents, enzymes, immuno-modulators or effectors, MHC molecules, antigens, chelators for radioactive labels, liposomes, transmembrane domains, viruses and/or cells, specifically, catoring and/or lated vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment, colon, stomach, pancreas, large/small intestine, overy, carvix, lung, colon, stomach, pancreas, large/small intestine, overy, cervix, lung, prostate, kidney and/or liver) and/or metastases (particularly to liver), the invention provide simple, reliable and efficient detection of tumours. They are specific for carcinoma and show almost no binding to healthy tissue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a chimeric antibody specific for human basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric antibody specific for human basic fibroblast growth factor, useful for preventing and treating pneumosilicosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse light chain variable region amino acid sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCPQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGVPDRFSGSGSGTDFTLKISRVBAEDLGVYYCFQGSHVPYTFGGGTKLEIX 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 555; DB 8; Length 11
Pred. No. 1.7e-42;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chimeric antibody; basic fibroblast growth factor; light chain variable region; pulmonary fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; SEQ ID NO 1; 17pp; Chinese
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                                                                                                                                                                                                                                                                                                                                                                                                                                              94.1%;
94.6%;
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Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEC21825;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEC2182
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                                                                                                                                                                                                                                                      20 DVLMTÓTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibody against the G glycoprotein of RSV with a variable region having a first and second domain from a VL and VH region, respectively, useful for treating respiratory syncytial virus (RSV) infections.
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                                                                                                                                                                                                                     DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G glycoprotein, respiratory syncytial virus;
respiratory syncytial virus infection, RSV; RSV infection; IC2; IgG1;
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of the chimeric IC2 kappa light chain in M13mp19 clone M609
fibroblast growth factor (bFGF) and its encoding gene. The chimeric antibody contains mouse variable regions and human constant regions human igglc. The antibody is useful for preventing and treating pneumosilicosis. The present sequence represents a mouse light chain variable region which can be used in a chimeric antibody of the
                                                                                                                                                                                                                                                                                       112
                                                                                                                                                                                                                                                                                                                      80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGGGTKLEIK 131
                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                       61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK
                                                                                                                                                      Length 139,
                                                                                                                                                  Score 555; DB 9; Length 13
Pred. No. 2.2e-42;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .19
/note= "Ig leader sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; SEQ ID NO 55; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYNE-) UNIV NEWCASTLE-UPON-TYNE.
                                                                                                                                                                                                                                                                                                                                                                                                            ADS88785 standard; protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-2004; 2004WO-GB001239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-2003; 2003GB-00006618
                                                                                                                                                      94.1%;
                                                                                                                                                                       94.68;
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                                                                                                                                                                     Local Similarity 94.6
nes 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADS88784
                                                                                                                       Sequence 139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004083373-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus sp.
Homo sapiens.
Chimeric.
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                                                                                       invention.
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                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chimeric
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Peptide
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Matches
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ADS88785
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Search completed: January 10, 2006, 20:44:13 Job time: 79.3134 secs

Wed Jan 11 09:35:23 2006

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2006
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January 10, 2006, 20:28:02; Search time 13.5124 Seconds (without alignments) 797.508 Million cell updates/sec Run on:

US-10-735-916A-54 590 1 DVLMTQIPLSLPVSLGDQAS......CFQGSHVPWTFGGGTKLEIK 112 score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			SUMMAKIES	
Result No.	Score	Query Match	Length	03	ID	Description
-	549	93.1	131	7	B39276	Ig light chain pre
7	547	92.7	112	~	A31807	kappa chain
m	547	92.7	219	N	PC4203	
4	546	92.5	110	~	S26335	Ig kappa chain V r
Ŋ	542		113	7	PL0203	anti-DNA autoantib
9	540	91.5	219	~	S52028	
7	536	90.8	118	7	PT0359	kappa
œ	536		131	~	B34904	kappa
σ	535	90.7		N	F27887	kappa chain
10	535	90.7		N	A32967	kappa chain
11	534	90.5		N	B31485	kappa
12	533	90.3	112	~	\$38719	light
13	532	90.2		N	C34904	kappa chain
14	531	90.0	225	~	JL0029	kappa
15	530	89.8		~	A27887	kappa chain
16	528	89.5		~	D28195	kappa
17	527	89.3		7	E27887	kappa
18	527	89.3		~	C27887	kappa
19	527	89.3		~	S16112	kappa chain V
20	526	89.5		~	B32967	kappa cha
21	526	89.2		~	B32513	kappa
22	524	88.8		~	A49715	kappa cha
23	522	88.5		~	S53750	ibody Fab
24	521	88.3	112	~	S32189	kappa cha
25	521	88.3		~	S38715	g kappa cha
26	521	88.3		~	S09259	g kappa
27	519	88.0		0	A34353	nti-peptide
28	518	87.8		~	2	g kappa ch
59	518	87.8	131	7	D34904	Ig kappa chain pre

		Ig light chain V r Ig kappa chain V r Ig kappa chain V r	kappa chair kappa chair :i-digoxin t	Ig kappa chain V r Ig kappa chain BrE Ig kappa chain pre	chain
	2 B27887 2 PL0257 2 PH1043			2 E32530 2 S67944 2 PT0178	2 S15673
			113 131 132	121	111
87.8 87.8	87.6 87.5 87.3	87.3 87.1 86.8	86.4 86.4 86.4	86.1 85.9 85.8	85.4
518	517 516 515	515 514 512	510 510 510	508 507 506	504
30	3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	35 36 37	8 6 4 8 6 0	4 4 4.	4 4 4 5

ALIGNMENTS

	Ig light chain precursor V-D-J region (6-19) - mouse C.Species: Mus musculus (house mouse)	C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Ja	Blon: D3270 nger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; 1	Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990 A,Title: Cryoglobulinemia induced by a mutrine Igg3 rheumatoid factor:
RESULT 1 B39276	Ig light chain	C;Date: 18-Oct-1991	R, Reininger, L	Proc. Natl. Ace A, Title: Cryog

: skin vasculitis a

Izui, S. an-2000

A, Reference number: A39276; MUID:91088540; PMID:2263605 A, Accession: B39276

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-131 <REI>

A;Cross-references: UNIPARC:UP10000115153; GB:M55313; NID:g198095; PIDN:AAA63385.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: immunoglobulin F;35-114/Domain: immunoglobulin homology <IMM>

ö Gaps ö Query Match 93.1%; Score 549; DB 2; Length 131; Best Local Similarity 93.8%; Pred. No. 3.3e-43; Matches 105; Conservative 2; Mismatches 5; Indels

20 DVLATQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 79 1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 셤 ò

9

61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112 ò g

Id kappa chain V region (PACI) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 20-3nl-1989 #sequence_revision 20-3nl-1989 #text_change 09-Jul-2004
C;Accession: A31807
R;Taub, R.; Gould, R.J.; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shatt.
C;Accession: A31807
A;Title: A monoclonal antibody against the platelet fibrinogen receptor contains a sequivalence number: A31807
A;Reference number: A31807
A;Reference number: A31807
A;Residues: Drellminary
A;Residues: 1-112 < TAU>
A;Residues: 1-112 < TAU>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology < INM>

92.7%; Score 547; DB 2; Length 112;

Query Match

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C;Accession: PL0203
R;Smith, R.G.; Voss Jr., E.W.
R;Smith, R.G.; Voss Jr., E.W.
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from A;Reference number: PL0198; MUID:90309768; PMID:2114528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-113 <SMI>
A;Cross-references: UNIPARC:UP10000113786; GB:X53643; NID:g50196; PIDN:CAA37694.1; PID:
ED:

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Cispecies: Mus musculus (house mouse)
Cjaceies: Mus musculus (house mouse)
Cjacession: 552028
Cjacession: 552028
Rivan Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;
Rivan Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;
A; Nebacription: Coordinate expression of antibody subunit genes yields high levels of fur
A; Reference number: 552028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPARC:UPI0000114B22; EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PJ C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVVMTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 60
                                                                                                                                                                       anti-DNA autoantibody BV17-31, kappa chain V region - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVLMTOIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCPQGSHVPFTFGSGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGGGTKLE 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: immunoglobulin V region; immunoglobulin homology;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 540; DB 2; Length 21
Pred. No. 3.8e-42;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 542; DB 2;
Pred. No. 1.2e-42;
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C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: immunoglobulin V region; immuno
F;16-95/Domain: immunoglobulin homology <nMm>
F;24-19/Region: complementarity-determining 1
F;55-61/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;94-102/Region: complementarity-determining F;101-113/Region: D region
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92.9%;
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92.0%;
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Best Local Similarity 92.94
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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A; Residues: 1-219 <VAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: PL0203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103;
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[Grappa chain (monoclonal antibody Maba34) - mouse (fragment)
[Grappa chain (monoclonal antibody Maba34)]
[Grappa chain and masculus (house mouse)]
[Gracession: PC4203]
[Gracession: PC4203]
[Grant 173, 257-259, 1996]
[Grant 173, 257-259]
[Grant 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIL
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Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
CiAccession: 826335
Afritie: Antibodies that are specific for a single amino acid interchange in a protein (A;Reference number: 826399; MUID:91341421; PMID:1908510
A;Recession: 826335
A;Residues: preliminary
A;Residues: 1-110 <STA>
A;Residues: 1-110 <STA>
A;Residues: 1-110 <STA>
A;Residues: inmunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
R;16-95/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
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Pred. No. 8.7e-43;
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Best Local Similarity 94.5%; Pred. No. 5.2e-43;
Matches 104; Conservative 2; Mismatches 4;
                                       4;
Pred. No. 4.3e-43;
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Best Local Similarity 93.8%;
Matches 105; Conservative
92.98;
                                    Matches 104; Conservative
Best Local Similarity
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90.5%; Score 534; DB
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[5] Species: Mus musculus (house mouse)
[6] Accession: B34904; H34903
[7] Ribedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
[7] Species: Musculus and antigen binding properties of idiotypically cross-real A; Reference number: A34903; MUID:90094387; PMID:2104617
[8] A; Reference number: A34904
[8] A; Reference number: A34903; MUID:90094387; PMID:2104617
[9] A; Residues: Preliminary; not compared with conceptual translation
[8] A; Residues: 1-131 < RED>
[9] A; Residues: 1-131 < RED>
[9] A; Residues: UNIPARC:UPI0000114FC8; GB:M32384; GB:J05237; GB:J05238; NID:G539656; CS:Usperfamily: immunoglobulin immunoglobulin homology
[9] Superfamily: immunoglobulin homology < IMM>
[9] F; 35-114/Domain: immunoglobulin homology < IMM>
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CiSpecies: Was musculus (house mouse)
CiSpecies: Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
CiSpecies: Species: Sp
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Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
Accession: PT0359
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                              C; Accession: Pr0359
R; Shefner, R.; Kleiner, G.; Turken, A.; Papazian, L.; Diamond, B.
J. Exp. Med. 173, 287-296, 1991
A; Title: A novel class of anti-DNA antibodies identified in BALB/c mice A; Reference number: Pr0352; MUID:91108325; PMID:1988536
A; Accession: Pr0359
A; Molecule type: mRNA
A; Residues: 1-118 cSHE>
A; Cross-references: UNIPROT:QSVCI6; UNIPARC:UP10000176AF2
A; Experimental source: strain BALB/c
C; Comment: This protein is an anti-double-stranded DNA antibody.
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; 19-98/Domain: immunoglobulin homology < IMM>
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Pred. No. 5.1e-42;
4; Mismatches 7; Indels
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Best Local Similarity 90.2%;
Matches 101; Conservative
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R;Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J. Biol. Chem. 264, 1565-1569, 1989
A;Title: Comparison of variable region primary structures within an anti-fluorescein ida
A;Reference number: A31485; MUID:89109167; PMID:2492278
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A; Cross-references: UNIPROT:099M37; UNIPARC:UPI0000176A19
A; Experimental source: strain Balb/c
A; Note: this sequence was determined from the germline gene
C; Comment: This chain was isolated from a hybridoma protein that binds influenza virus
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
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C;Species: Mus musculus (house mouse)
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF
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                                                                                                                                                                                                                                                                                                                        90.7%; Score 535; DB 2; Length 112; 92.0%; Pred. No. 5.3e-42; tive 2; Mismatches 7; Indels
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Gaps

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4; Mismatches

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Matches 100; Conservative
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 27-Ul-1990 #text_change 09-Jul-2004
C; Accession: C34904; I31485; 1990
A; Title: Active site structure and antigen binding properties of idiotypically cross-res
A; Reference number: A44903; MulD:90094387; PMID:2104617
A; Accession: C34904
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-131 - RED>
A; Cross-references: UNIPROT: Q8VCI6; UNIPARC: UPI00001767A8
B; Bedayk, W. D: Johnson, L. S.; Riordan, G. S.; Voss Jr., E. W.
J. Biol. Chem. 264, 1565-1569, 1989
A; Title: Comparison of variable region primary structures within an anti-fluorescein idi
A; Reference number: A31485; MulD:89109167; PMID:2492278
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C:Species: Mus musculus (house)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
R;Cimcanis, A.Y.
submitted to the EMBL Data Library, November 1993
A;Reference number: S38713
A;Reference number: S38713
A;Accession: S38719
A;Accession: S38719
A;Residues: 1-112 <CIMA
A;Residues: 1-112 <CIMA
A;Residues: 1-112 <CIMA
A;Residues: 1-112 <CIMA
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: immunoglobulin homology <IMM>
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                         0; Gaps
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A;Molecule type: protein
A;Residues: 20-52 <BE2-
A;Cross-dues: UNIPARC:UPI00001767A9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                      Indels
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Pred. No. 1.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.3%; Score 533; DB 2; ilarity 90.2%; Pred. No. 8.1e-42; Conservative 5; Mismatches 6
    6.5e-42;
                      6; Mismatches
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  Pred. No.
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89.3%;
89.3%;
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                      100; Conservative
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Matches 101; Conserv
Best Local Similarity
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                      Matches
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A; Residues: 1-225 acdft.
A; Residues: 1-225 acdft.
A; Cross-references: UNIPROT:Q99M37; UNIPARC:UPI000017697F
A; Cross-references: UNIPROT:Q99M37; UNIPARC:UPI000017697F
A; Cross-references: UNIPROT:Q99M37; UNIPARC:UPI000017697F
A; Cross-references: UNIPROT:Q99M37; UNIPARC:UPI000017697F
A; Cross-references: UNIPROT:Q99M37; UNIPARC:UPI000016 as Pro., ACC for residue 132
A; Note: the nucleotide sequence shown is inconsistent with authors' translation because ect except for four positions shown above
C; Comment: The protein is an anti-phosphorylcholine antibody.
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin #status predicted < LLC>
F; 7-225; Product: Ig kappa chain #status predicted < LLC>
F; 7-106; Domain: V region #status predicted < LLC>
F; 107-119; Domain: C region #status predicted < LCC>
F; 120-225; Domain: C region #status predicted < COR>
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R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
BMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a dA;Reference number: A91043; MUID:86300658; PMID:2427335
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A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
A;Note: this sequence was isolated from a hybridoma protein that binds influenza virus h
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphosphor A,Reference number: JL0029; MUID:88171315; PMID:3127529
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                                                                                                                  DVVWIQTPLSLPVSLGDQASFSCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain precursor (RP93) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: JL0029
R;Chien, N.C.; Pollock, R.R.; Desaymard, C.; Scharff, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain V region (H37-60) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
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                                                                       DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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                                                                                                                                                                                                                             YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                 80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPWTFGGGTKLEIK 131
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8; Indels
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Pred. No. 2.6e-41;
5; Mismatches 7;
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Pred. No. 1.5e-41;
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Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
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1 DVLATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60 :		
PVSLGE PVSLGE	QASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60	OQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF 60
	PVSLGDQASISCR	PVSLGDQASISCR

⁶¹ SGVPDRESGSGSTDFTLRISSVBABEDGVYYFGGSHVPWTFGGGTKLBIK 112

61 SGVPDRFSGSGSGTDFTLRISSRLBABEDLGVYFCSGSHVPWTFGGGTKLBIK 112

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1 DVLMTQIPLSLPVSLGDQAS......CFQGSHVPWTFGGGTKLEIK 112
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Gapop 10.0 , Gapext 0.5
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Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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91.7%; Score 541; DB 2; Length 248;
Best Local Similarity 92.9%; Pred. No. 1.4e-49;
Matches 104; Conservative 2; Mismatches 6; Indels
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QFEZIO;
10-MAY-2005 (TERMELrel. 30, Created)
10-MAY-2005 (TERMELrel. 30, Last sequence update)
10-MAY-2005 (TERMELrel. 30, Last annotation update)
Kappa light chain variable region (Fragment).
Name=IgG1 anti-TS1 VL;
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065207;

25-0CT-2004 (TrEMBLrel. 28, C

25-0CT-2004 (TrEMBLrel. 28, L

25-0CT-2004 (TrEMBLrel. 28, L

B3 (FV) - PE40 (Fragment).
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InterPro; IPR007110; Ig-like.
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           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
                                                                                                                            NUCLECTIDE SEQUENCE.
Erlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;
Studies of the interactions between the anticytokeratin 8 monoclonal
antibody TS1, its antigen and its anti-idiotypic antibody alphaTS1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Buarchontogliree, Gliree, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                            Erlandsson A.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ884575; CAI56337.1; -; mRNA.

InterPro; IPR003599; IG.

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

Fam: PF07666; V = et.;

SMART; SM00409; IG. 1.

SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12560 MW; E4D3BF3D63E88007 CRC64;
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87.6%; Pred. No. 8.1e-47;
ive 6; Mismatches 7;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; Q99M37; 1191.
Ensembl; ENSMUSG0000055315; Mus musculus.
                                                                                                                                                                                                                J. Mol. Recognit. 16:157-163(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=83178921; Pubmed=6404298;
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Matches 99; Conservative
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  musculus (Mouse).
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                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=86136012; PubMed=3937730; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system."; EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kappa chain (Fragment).
Mus musculus (Mouso)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YGVPDRFSGSGGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGVPDRFSGSGSGTDFTLKISRVEAEDLGIYFCSQTTHVPPTFGGGTKLEIK 112
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv. 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Monoclonal antibody.
                                                                                                                                    Complementarity-determining-1.
                                                                                                                                                                                Complementarity-determining-2.
                                                                                                                                                                                                                            Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 112
112 AA; 12266 MW; C844B7881A89C18A CRC64;
                                                                                                                                                                                                                                                                                                                     12273 MW; F9F39CE949A84C2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          Score 510; DB 1;
Pred. No. 1.1e-46;
5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.2%; Score 491; DB 2;
83.0%; Pred. No. 1.2e-44;
iive 8; Mismatches 11;
                                                                                                                                                                                                                                                                      By similarity.
                                                                                                                                                           Framework-2
                                                                                                                                                                                                       Framework-3
                                                                                                               Framework-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE OF 108-109.
                                                                                                                                                                                                                                                                                                                                                                 86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q53VP8 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           98; Conservative
                                                                                                                                      39
54
61
102
112
93
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                                                                                                                                                                                                                                                                                                                     113 AA;
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NON TER
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Local Similarity 78.6%
nes 88; Conservative
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QBTCDO;
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74
74
113
113
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113
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133 AA;
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                             Kipp B., Schlaak M., Becker W.M.;
"Cloning and expression of a recombinant mouse Fab-fragment recognizing a defined linear epitope of Chironomus thummi thummi major allergen Chi t I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ELVMTQSPLSLSVSLGDQASISCRSSQSLVHTNGNTYLHWYLQKPGLSPKLLIYIVSNRF
                                                                        25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Kappa light chain C region (Fragment).
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.
"Human immunoglobulin kappa light chain genes of subgroups II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.9%; Score 489; DB 2; Length 219; 83.9%; Pred. No. 4.5e-44; ive 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P06310;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-MAX-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-II region RPMI 6410 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                          Int. Ärch. Allergy Immunol. 110:348-353(1996).
EMBL; Z37499; CAA85724.1; -; mRNA.
SMR; Q65ZCO; 1-219.
                                        219 AA
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                                        PRT;
                                                                                                                                                                                                                                                                                                             MEDLINE=96319505; PubMed=8768802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003597; IG_c1.
InterPro; IPR003506; IG_MG.
InterPro; IPR003506; IG_WHC.
InterPro; IPR003596; IG_WHC.
InterPro; IPR003596; IG_V.
Pfam; PF07654; C1-8et; I.
SWART; SM00407; IG_c1; I.
SWART; SM00407; IG_c1; I.
PROSITE; PS00395; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; I.
                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
STPAIN-Balb/c; TISSUE-Spleen;
                                        QESZCO_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94; Conservative
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                                                                                                                                                                                                               Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                      MOUSE
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KV2F HUMAN
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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X MEDINEE-2238855; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.

XA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

RA Brownstein M.J., Uddin T.B., Toshlyviki S., Carninori P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 DVVWTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRLIYKVSNRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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Complementarity-determining-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Framework-3.
Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                        Ensembl; ENGGO0000173758; Homo sapiens.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0005825; P:antigen binding; NAS.
GO; GO:0006555; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGV; I.
PROSITE; PSS0355; IG IKKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14707 MW; 513CCAF3673009EE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
                                                                                                                                                                                                               EMBL; Z00020; CAA77315.1; -; Genomic_DNA.
PIR; A01890; KZHURP.
HSSP; Q99M37; 1191.
SMR; P06310; 21-133.
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SGVPDRFSGSGSGTDFTLKITRVEAEDVGVYFCMQGTHWPSTFGQGTKLEIK 132

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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=8258341;
Klein R., Jaenichen R., Zachau H.G.;
"Expressed human immunoglobulin kappa genes and their hypermutation.";
Eur. J. Immunol. 23:3248-3262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wagner S.D., Luzzatto L.;
"V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                Hirabayashi Y., Munakata Y., Sasaki T., Sano H.; Munakata P., Sasaki T., Sano H.; Muraiable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-associated idiotype.", Nucleic Acids Res. 20:2601-0(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                     Lautner-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F., Thiebe R., Zocher I., Zachau H.G.; "The human immunoglobulin kappa locus. Characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.8%; Score 453; DB 2; Length 23 Best Local Similarity 76.8%; Pred. No. 3.7e-40; Matches 86; Conservative 13; Mismatches 13; Indels
                                                                                                                                                                                            TISSUE=Lung;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00230; IG_MHC; UNKNOWN 1.
Hypothetical protein; Immunoglobulin domain.
SEQUENCE 239 AA; 26235 WW; FACEDC3A3B03871D CRC64;
                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUI. J. Immunol. 23:391-397(1993).
EMBL; BC022362; AAH22362.1; -; mRNA.
PIR; S22689; S22658.
PIR; S34095; S34095.
PIR; S40324; S40324.
PIR; S40374; S40374.
PIR; S42267; S42267.
PIR; S42267; S42267.
PIR; S42267; S42267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Immunol. 22:1023-1029(1992)
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP07654; C1-8et; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            duplicated A regions."
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           somatic mutation."
                                                                                                                                                                                                                                                                                 PubMed=1598223;
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PubMed=1601042;
PubMed=1601042;
Hubber C., Klobeck H.G., Zachau H.G.;
Hubber C., Klobeck H.G., Zachau H.G.;
Hubber C., Kappa-J kappa-J kappa coding jointcombination after formation of a productive V kappa-J kappa coding joint.";

Eur. J. Immunol. 22.1561-1565 (1992).

EMBL; AR035034; AAD56270.1; -; mRNA.

PIR; 849002; B49002.
                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                  PubMed=1322670;
Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr,
Gaskin F., Fu S.M.;
"A rheumatcid factor from a normal individual encoded by VH2 and V
kappa II gene segments.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wagner S.D., Luzzatto L.; "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
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                                                                                                                                                                                                                                                                                    "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                 MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 114;
                                          01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.5%; Score 451.5; DB 277.9%; Pred. No. 2.2e-40; ive 10; Mismatches 14
                                                                                                                                                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192(1998).
              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Immunol. 23:391-397(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Arthritis Rheum. 35:900-904 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 77.9%
nes 88; Conservative
             Q9UL80_HUMAN PRELIMINARY;
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PIR; S34095; S34095.
HSSP; P01625; 1LVE.
SMR; Q9UL80; 1-114.
                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            somatic mutation.
                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                            (Fragment)
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HUMAN
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Homo sapiens
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RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Whtl model.

RC Expression driven by an MMTV-LTR enhancer.;

RX Strausberg RL., Feligold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

RA Appleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.B., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rahas S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Toung A.C., Shevchenko Y., Bouffard G.G.,

RA Rahas R.W., Touchman J.W., Green B.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schwutz R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Generation and initial analysis of more than 15,000 full-length human and mouse cDNA semences."
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                                                                                                                                                                                                                                                                                       Mus mušculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPPWTFGQGTKVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model
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PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SEQUENCE 239 AA; Z6302 MW; 98FC4BA8EB404215 CRC64;
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                                                                                                                                                                                         Last sequence update)
Last annotation update)
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NIH MGC Project;
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SMR; O58E08; 21-239.
GO; GO:0003823; F:antigen binding; IEA.
InterPro; IPR003599; IG.
InterPro; IPR007510; Ig-like.
InterPro; IPR003597; Ig C1.
InterPro; IPR003596; Ig MHC.
InterPro; IPR003596; Ig WHC.
Pfam; PF07654; C1-8et; I.
                                                                                                                                                                     Created)
                                                                                                                                                             10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences."
                                                                                                058EU8_MOUSE PRELIMINARY;
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SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 1.
SMART; SM00406; IGC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CZECH II;
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REDULINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Rausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rluaner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschenk C., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robark S.A., McZwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rodriques S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Cenerzation and initial analysis of more than 15,000 full-length human
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063599; AAH63599.1; -; mRNA.
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Last sequence update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SMR; Q6P491; 21-237.
INTERPRO; IPRO031599; IG.
INTERPRO; IPR0031599; IG.
INTERPRO; IPR003106; IG_IL.
INTERPRO; IPR003106; IG_NHC.
INTERPRO; IPR003106; IG_V.
Pfan; PP07654; C1-8et; I.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
PROSITE; PS00815; IG_ILKE; 2.
PROSITE; PS00815; IG_ILKE; 2.
                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypothetical protein.
                                                                                                                                                                                                                                    QEP491 HUMAN PRELIMINARY;
QEP491;
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SEQUENCE 239 AA: 2
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Best Local Similarity
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S40357; S40357.

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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIdusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Aptich R.F., Jordan H., Moore T., Max S.I., Wang J., Hatch F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A blatchen M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.B., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raha, Miling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

And mouse Chara A. Schein J.E., Jones S.J.M., Marra M.A.;

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=1601042;
Huber C., Klobeck H.G., Zachau H.G.;
Huber C., Klobeck H.G., Zachau H.G.;
"Ongoing V kappa-J kappa recombination after formation of a productive V kappa-J kappa coding joint.";
Eur. J. Immunol. 22:1561-1565(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein R., Jaenichen R., Zachau H.G.;
"Expressed human immunoglobulin kappa genes and their hypermutation.";
Bur. J. Immunol. 23:3248-3262(1993).
EMBL; BC030814; AAH30814.1; -; mRNA.
PIR; S23638; S23638.
PIR; S34091; S34091.
PIR; $40342; S40342.
                                                                                                                                                                                                                              Name=IGKV1-5;
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=8436174;
Wagner S.D., Luzzatto L.;
"V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                  61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Director MGC Project;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 somatic mutation.";
Eur. J. Immunol. 23:391-397(1993)
                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."
                                                                                                                  QBNEKO HUMAN PRELIMINARY;
QBNEKO;
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                                                                                                                                                                                                              IGKV1-5 protein.
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                     1 DVLATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-84191506; PubMed=6325927;
Klobeck H.G., Solomon A., Zachau H.G.;
"Contribution of human V kappa II germ-line genes to light-chain
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Framework-2. 
Complementarity-determining-2.
                                                                                                                                                                                                                                            ch 75.3%; Score 444; DB 2; Length 239; 1. Similarity 75.0%; Pred. No. 3.4e-39; 84; Conservative 11; Mismatches 17; Indels
HSSP, P01834; 1172.

SMR; QNNEKO; 21-237.

InterPro; IPR0031010; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003597; Ig_U.

InterPro; IPR003596; Ig_W.

Pfam; PP0764; IC. set; I.

SMART; SM00406; IGV; I.

PROSITE; PS50835; IG_LIKE; 2.

PROSITE; PS50290; IG_MHC; UNKNOWN_I.

Immunoglobulin domain.

SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552COA CRC64;
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SMR, P063309; 5-117.

GO; GO:0003823; F:antigen binding; NAS.

GO; GO:0003823; F:antigen binding; NAS.

GO; GO:0006955; P:immune response; NAS.

InterPro; IPR00110; Ig-like.

InterPro; IPR00110; Ig-like.

SMART; SM00406; IGV; 1.

PROSTIE; PS:0035; IG LIKE; 1.

Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-II region GM607 precursor (Fragment).
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Framework-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
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P06309;
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                                                                                                                                             DIVMIQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGSNRA 64
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                               1 DVLATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=73166638; PubMed=4700495; Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F., Glenner G.G.; Structural identity of Bence Jones and amyloid fibril proteins in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          patient with plasma cell dyscrasia and amyloidosis.";
J. Glin. Invest. 52:1276-1281(1973)
-!- MISCELLANEOUS: The anajor amyloid protein appears to be identical
with the Bence Jones protein isolated from the same patient.
-!- MISCELLANEOUS: This protein was isolated from the urine of a
patient with plasma cell dyscrasia and amyloidosis.
-!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=74148480; PubMed=4596149;
Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
"Amino acid sequence of a kappa Bence Jones protein from a case of
                                                                                                                                                                                           SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGLQTPQTFGQGTKVEIK 116
                                                                                                                                                                                61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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                                                                                 Length 117;
 Complementarity-determining-3. Framework-4.
                                                                                                       18; Indels
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PROSTE; PSS0835; IG_LIKE; 1.
Amyloid; Bence-Jones protein; Direct protein sequencing;
Immunoglobulin domain; Immunoglobulin V region.
                                                          12664 MW; 92C57DC719E558B1 CRC64;
                                                                                  Score 441; DB 1;
Pred. No. 3.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW)
                                                                                                                                                                                                                                                                                        21.JUL-1986 (Rel. 01, Created)
21.JUL-1986 (Rel. 01, Last sequence update)
21.JUL-1986 (Rel. 01, Last annotation update)
19 kappa chain V-II region TEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005576; C:extracellular region; NAS. GO; GO:0003823; F:entrigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig_v.
                                                                                                        9; Mismatches
                       By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 12:3763-3780(1973).
                                                                                 74.78;
75.98;
                                                                                                          Conservative
                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           primary amyloidosis.";
                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                    Query Match
Best Local Similarity
Local 85; Conserve
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                                                         117 AA;
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SMR; P01617; 1-113.
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                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aebersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
"Murine V kappa 25 and V kappa 27 amino-acid sequences of C57B1/6
origin: monoclonal antibodies 17829.1 and 22825.1 specific for the
group A-streptococcal polysaccharide.";
Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
-i- FUNCTION: Anti-streptococcal group A carbohydrate antibody.
                                                                                                                                                                                                                                                                                                                                                                                               61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv. 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
Interpro; Immunoglobulin V region.
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Pred. No. 6.2e-39;
12; Mismatches 17; Indels
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Complementarity-determining-3.
                   Complementarity-determining-1.
                                                            Complementarity-determining-2.
                                                                                                    Complementarity-determining-3
                                                                                                                                                                                    12316 MW; 0C3C38F81F1843CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
19-MAY-2005 (Rel. 47, Last annotation update)
19 kappa chain V-II region 17829.1.
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                                                                                                                                               By similarity.
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                                           Framework-2.
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MEDLINE=85128968; PubMed=6441768;
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                                                                                                                                                                                                                              74.2%;
                                                                                                                                                                                                                                                   74.18;
                                                                                                                                                                                                                                                                       83; Conservative
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HSSP, Q99M37; 119I.
SMR; P03976; 1-113.
                                                                                                                                                                                    113 AA;
                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=10090;
  PROTEIN SEQUENCE
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                                                                                                                                                                                                                1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Riesen W.F., Jaton J.-C.;
"Variable region sequence of the light chain from a Waldenstroms IgM
with specificity for phosphorylcholine.";
Biochemistry 15:3829-3833(1976).
-I- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
macroglobulin that binds phosphorylcholine.
                                                                                                                                                                                                                                                                                                61 YGVPDRFSGSGSGTDFTLKISSVBAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
                                                             Length 113;
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Framework-4.
                                                          72.2%; Score 426; DB 1; Length 11 ilarity 71.4%; Pred. No. 1.2e-37; Conservative 14; Mismatches 18; Indels
113 AA; 12390 MW; 4E93797046F8DB33 CRC64;
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GO; 00:000582; F:antigen binding; NAS.
GO; 00:000585; P:immune response; NAS.
InterPro; IPR00710; Ig-like.
InterPro; IPR03596; Ig-v.
SMART; SM00406; IGv; I.
PROSITE; PS20835; IG IKE; I.
Direct protein sequencing; Immunoglobulin domain;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-II region FR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin V region.
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les 80; Conserv
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SMR; P01615; 1-109.
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